

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGCGCCGAGGACCTGGAGCTCCGCGTGCCTCTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAAACAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCTGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT
GTGTGAAGAACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCTACAGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGCAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTTCAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCTGCACTGGACAGCGGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCACTTGTTTATTGCACTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAATC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT
AACCTTGAAAGAGGAACTTGTTTAGGTACCTTCTGAGGCGAAAGAACAGCTGTGGAATG
TGTGTCAGTTAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDATAKNFGGGNTAWEKTLISKYESSSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFVCVKTCLKVCCSPGTYPGDCCLACQGGSQRPSCG
NGHCSDGDSRQGDGSCRCMHMGYQGFLCTDCMDGYFSSLRNETHSICTACDESCKTCSTGLTNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAQAQCKNANGSYTCECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCPCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTTGCG
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCTGAGCAGCATGGGCCCGGAGGAGCGCCTTC
CCTGCCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTTGAAGAAGATATCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAAATGCCAGCTATTCCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCCTGTCCTTGCCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAATTCGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCT
TCTTTAAAACATGTCAACAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTAAATGGAGGGACC
TGTTTCTACCTTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCCACAACCTGTGCGAAATGGAGGTAATGCATTGGTAAAAGCAAAATGTAAAGTGT
CCAAAGGTTACCAAGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGTGGTGCACAT
GGAACCTGCCATGAACCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCCACCTCAGGCAGC
ACACGCCTTCACTTAAAAGGCCGAGGAGCGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACCTCCGACATCTGAAACGTTTTAAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA
TGTGTTGAATGTTCAAATAATGTTTCATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCTCTTTTAAAGTTTCTTAAGTACGCTCTAG
CATGATGGTATAGATTTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTCAAATTTACAATGCATTTATGGT
GTCTGGGGGCGAGGGAACATCAGAAAAGGTTAAATTTGGGCAAAAATGCCTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTGAGATTTTAGAT
GTTTGTTACATTTTTAAAAATGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACC
TTACCATATTCCAGAGATTTCAGTATTAAAAAATAAATAAATAAATAAATAAATAAATAAATAA
AAACAATATAATATATTCTAAACCAATGAAATAGGGAATATAATGTATGAACCTTTTGCAT
TGGCTTGAAGCAATATAATATATTGTAAACAAAACAGACTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAATAAATAA
AAAAAATAAATAAATAAATAAAGGCGCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAIFYEFLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGCCCCAGGAGCCACC**AT**TGGCGCATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG
GAGCTAGCACCCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCGCGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCGGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGGCGTGCCACCCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTTTGGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCCAGGAAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTTCTGGGGCATGACCCTGGAT**GA**GGGCAATTCGCTACCGCCTGGGCACCA
TCCGCCCCTCTTCTCGGTTCATGAACATGTCATGAAATTTATACAGTGCTGAACCCAGGGGAG
GTGCTTCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCAACCTGATTATGAGCCTCTTGA
CCAAGGCAACTGTGCAAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCCCCAGAACCTGCTGTCTTGTGAC
ACCCACAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCTGGTGGTTCTCGCGTCG
CCGAGGGGTGGTGTCTGACCATTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCCGGGCAAGCGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGTGCACTCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCGAGAGATACCGCCCGCATGGGACCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGA CTGCGGCCAACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGGGCACTTCCGCATCGTGCGCGCGCTCAATGAGTGCGACATCGAG
AGCTTCGTGCTGGGCGTCTGGGGCGCGTGGGCATGGAGGACATGGGTCACTAGGCTG
CGGGCACACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCAGCCTCGCCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCGGCGCGGGTTCCGCTGACGCAGCGCCCCCGCCTGGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCAGGCCTCTGGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCCAATCCCGTATTCTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCCAGGTTGGAGTGCACTGGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA
AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC
TAATTTTTGTATTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCTGTATTCTTATTCTTCAGATATTTATTTTCTTTTCACTGTTTTAAAA
TAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQDLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTAACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCTTGCCTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCCG
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAA CATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCAGTGGGAGCCTGTCCTGGTTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCCCTGACCCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCCTGCAGATGGCCCCCTCCAACCCTCTCTGTGCTGTGTTTC
CATGGCCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARTSRAVTPTCATPAGMPCSRLLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPPQASVPLLLTDLAQWEPVLVPEAHFNASLTMYVCTPVPHDPMPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFFAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCG**AT**GGGAGCCGCCCGCTGCTGCCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGCGCAAGCA
CGTGCGAGGTACCGGGCGTTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCAGGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCCCTCCCCAACACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCTCACG**TAG**TCTGGGAGGCAGGGGCGAGCAGCCCTGGGCCGCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGCAAGCATCCGAGCCCCAGCTGGGAAGGGGAGGCCAGTCCCC
CCCAGGGGCGGCTGGCACAGTGTCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGTGAAAGGTGAGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCAACTCCTCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTGTTGTTGTTTTCAGGAAAAAGAAAGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCTCTGC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVFTEIVLE
NNYTAFQONARHEGWMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAAAGAGGGGCAACACAGGCTGTAAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGTATTTTGGCTGTTTATTTTTTTTTCTTTTTCTTTTTCCCAACACATGTATTTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCCT
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAACTCCTGGCCTGCC
CTAGTGTGTGCGGTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAACACCAATTAATAATGC
TGGATTTTCTGCAAGTGCACATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTTCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAA
AATATTAGACCATTTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTTGGGCTTCCCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTTCGTGTCC
CACCCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCCAGAT
AAACCACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTTGTGACTGTCAGTATTAATGGGTCCAGAAATGGCTCAA
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTTCATGTGCCAAGGTCTGAACAAGTCCGGG
GGATGGCCGTGAGGGAATTAAATATGAATCTTTTGTCTGTCCACCACGACCCCCGGCCTG
CCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCTCTCTAT
TCCAAACCTTAGCAGAAGCTACAGCCCTCCAACCTCTACCACATCGAAACTTCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTTACCGTGATGGCATA
CAAATCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAAGGC
CACCACCCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGGGTGATATTT
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGTCATATGCACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAATACAACCGGGGCCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACTCCATCCTGGAGATGACAGAAACAGTTTTTCAGATCGTCTCTTAAATAACGAT
CAACTCTTAAAGGAGATTTGAGACTGCAGCCATTTACACCCCAAATGGGGGCATTAATTA
CACAGACTGCCATATCCCCAACCAATGCGATATGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAAATTAGACTCTTGAGAA
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
TTGTGCATTTGAATACTCTGTAATTTATACGGGTACTATATAATGGGATTTAAAAAAGTG
CTATCTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACTCTTTGCTTTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVLYLGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLLDINSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSI VRNSLSHPFPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKNVTEWLKYIPSSLNVRGFMCCQPEQVRGMVRELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTTTSKLPTIPDWDGRERVTPPISERIQLSIFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHEMGSFPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKYNRRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

A CTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCGAGAGCGAGAAGCTGGGGCTCCGCTCTCGCTCCCAACGAGCG
 ATCCCGAGGAGAGCCCGCGGCCCTCGGCGAGGCGGAAGAGGCCGACGAGGAAGACCCGGGTGGCTCGGCCCTTGCC
 TCGCTTCCAGGCGCGCGCGGCTGCAGCCTTGCCCTCTTGCTCGCCTTGAAAATGGAAAAAGATGCTCGCAGGCT
 GCTTTCTGCTGATCTCGGACAGATCGTCTCTCTCGGCGAGGCGCAGGGAGCGGTACAGTGGGAGGTCCATCT
 CTAGGGGCGAGACACGCTGGACCCACCCGCGAGACGGGCCCTTCTGGAGAGTTCTGTGAGAACCAAGCGGGCGAGCC
 TGTTTTCATCATTTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAAGGTCAAGGAGTTTCATCGTGGACA
 TCTTGCAATTCTTGGACATTGGTCTCGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCAGTGTCAAGAAATG
 AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG
 GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGGCCGCCCTCGA
 GGGAGAATGTGCCACGGGTGATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA
 AGGCACGGGACACGGGCTATCTAATCTTTGCCATTTGTTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
 GAGTGGAGCCCATGAGGACCATGTCCTCTCTGTGGCCAAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC
 AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG
 GCTCATACGTTCTGAGGTGCAAAACAGGCTACATTTCAACTCGGATCAGACGACTTGCAGAAATCCAGGATCTGT
 GTGCCATGGAGGACCAACAATGTGAGAGGCTCTGTGTGAATGTGCCGGGCTCTCTCGTCTGCCAGTGCTACAGT
 GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCTCAGAAAAACCAAGGATGTGAAC
 ATGAGTGTGTAATGCTGATGGCTCTTACCTTTGCCAGTGCCATGAAGGATTGTCTTTAAACCCAGATGAAAAAA
 CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGCTGTGAGCATGAGTGTCTCAACATGGAGGAGAGCT
 ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCATCTGTGCAC
 AGCAGGACCTGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTCTGTCTCGCAGTGTCTCAGAGGCTTCC
 TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCTGTGAGTACCATTGTTGTGAATATCTCTCT
 GTGTCAACATGGACAGATCCTTTGCCCTGTCACTGTCTGAGGGACACGCTGCCGAGCGATGGGAAGACGCTGTG
 CAAAATTTGGACTCTTGTGCTCTGGGGGACACCGTGTGTGAACATTCTGTGTGAAGCAGTGAAGATTCTGTTGTGT
 GCCAGTGTCTTGAAGGTTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAGATGTCTGCCAAGCTATAG
 ACCATGGCTGTGAACACATTTGTGTGAACAGTGAAGCTCATAACGCTGCGAGTGTCTGGAGGGATTCCGGCTCG
 CTGAGGATGGGAACCGCTGCCAAGGAAGGATGTCTGCAAAATCAACCCACCATGGCTGCGACACATTTGTGTTA
 ATAATGGGAATTCCTACATCTGCAAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGCTGCAAGAAAT
 GCACTGAAGGCCCAATTGACCTGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAAGTGTG
 TGAAGCAGTTTGTCACTGGAATTTATAGATTCTTTGACAAATTTCCCCCAAGCCGCTCGAGTGGGGCTGCTCCAGT
 ATTCACACAGGTCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAGCAAGACATGTTTGAAGAGAGTCTT
 ACATGAAATACATGGGAAGGGCTCTATGACTGGGCTGGCCGTGAACACATGTTTGAAGAGAATTTTACCCAG
 GAGAAGGGCCAGGCCCTTTCCACAAGGGTGGCCAGAGCAGCCATTGTGTTACCCGACGGACGGGCTCAGGATG
 ACGTCTCCGATGGGGCAGTAAAGCCAAAGCCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAGCCATTG
 AGGAGGAACCTCAAGAGATTGCTCTGAGCCCAACAAACAGCATCTCTCTATGCCGAAGACTTCAGCAAAATGG
 ATGAGATAAGTGAAGAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
 CAGGGGAACCTGCCAAAACGGTCCAAACAGCCCAACAGAATCTGAGCCAGTACCCTAATATCCAAAGACCTACTTT
 CCTGTTCTAATTTTGCAGTGTCAACACAGATATCTGTTTGAAGAAAGACAATCTTTACGGTCTACACAAAAGCTTT
 CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAAATGTGAAGAACTTATAATGT
 TCCAGAACCTTGCAAAACGAAGAAGTGAAGAAAATTAACAACAGCGCTTGAAGAAATGACACAGAGAATGGGAAGCC
 TGGAAAATCGCTGAGATACAGATGAAGATTAGAAAATCGCGACACATTTGTAGTCATTGTATCAACGGATTACAAT
 GAACGCACTGACAGAGCCCAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACAAATCAGTACTGA
 GAAACCTGGTTTGCACAGAACCAAGACAAAGATATACACTAATCTGTATAAATTTACTAGGAAAAAATCTCT
 TCAGAAATCTAAGATGAATTTACAGGTGAGAAATGAATAAGCTATGCAAGGATTTTGTGAATATCTGTGGACAC
 AACTGTCTCTCGCTCATCTCGCTTAGTGTGCAATCTATTGACTATACGATAAAGTTTGCACAGTCTTACTTT
 CTGTAGAACACTGGCCATAGGAATGCTGTTTTTTGTACTGGACTTACCTTGATATATGTATATGGATGTATG
 CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAAATTTAAATTCACCACCTTCAG

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FIGURE 15

MEKMLAGCFLLLILGQIVLLPAEARERSRGRSISRGRHARTHPTOTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKRSEVERAV
KMRHLSLTGTMTGLAIQYALNIAPFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVVCRCRKQGYILNSDQTTCRIQDLAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFIL
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDSALGDHGCE
HSCVSSSEDSFVCQCPEGYILREDGKTCRRKDVCAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDIEISEKLKKGICEALESDGRQDS
PAGELPKTVQOPTSEPVTTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
BEKHDQCKCENLIMFQNLANEVVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCTGGTGACCACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCAC TTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGTCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCTGCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGTCTGGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTAACACCGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGACCTGCCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTGAGGCTGGCTTGGTAGGTTTTTACTGGGGCAGAGGATAGGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTTCATTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSTKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGFPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCCTGCGGCCACCGCCAATGAAACGCTCCCGCTCCTAGTGGTTTTTTCCACTTTG
TTGAATTGTTCTTACTCAAATTCACCAAGACACCTTGTCTCCCAAATGC AAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCACATGGGATTTTCAGGAAATGGTGTACAA
TTTTGTGAAGATGATAATGAATGTGGAATTTAACTCAGTCCCTGGCGAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGC AAATGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAATAAACTTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTTTGCTACAGAAAGTCTATAGAAATTCGTGACAGATCTTTCAACAACAGA
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAACA
CTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAAT
AATTTTGTTC AAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
AAAAGACCACAGAGTTTGTATCAAAATTCACCGGATATAGCTCTCAAAGTTTTCTTTTTGTAT
TCATATAACATGAACATATTCACCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGTCTCTTGTCTTCATCATCTGACAACCTCTTATTGAAACCTCAA AATTATGAT
AATCTGAAGAGGAGGAAGAGTCAATCTTCAGTAATTTCACTCAATGAGCTCAAACCC
ACCCACATTATATGAACCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATA
GGTATAGGAGTCTATGTGCATTTTGAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATCTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTTTGC AATTTTGTATGTCCTCTGGTCTCTCCATTGGTATTAAAGATTATAATATTC
TTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTT
ACCTTCTGGTTCTTCAGTGA AATTC AAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG
TAGCCTATTCTTGTCTGAACCTGTTTCTTCTGTTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTTGCCGGACTGCTACACTACTTCTTTTAGCTGCTTTTGCATGGATGTG
ATTGAAGGCATACATCTCTATCTCATTTGTTGTGGGTGTCTATCTACAACAAGGGATTTTTC
CAAGAATTTTATATCTTTGGCTATCTAAGCCCAGCCGTTGGTAGTTTGGATTTTCGGCAGCAC
TAGGATACAGATATTATGGCACAAACCAAGTATGTTGGCTTAGCACCGGAAAAACAATTTATT
TGGAGTTTATAGGACCAGCATGCCTAATCATTTCTGTTAATCTCTTGGCTTTTGGAGTCAT
CATATACAAAGTTTTCGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACA
TAAGGTCTTGTGCAAGAGGAGCCTCGCTCTTCTGTTCTCTCTCGCACACACCTGGATCTTT
GGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGC
TTTCCAGGGGATGTTTCA TTTTATCTCTGTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAAATGTC CCGTGTGTTTGGATGTTTAAGGTTAAACATAGAGAAATG
GTGGATAATTACAACCTGCACAAAAATAAAAAATTC AAGCTGTGGATGACCAATGTATAAAAA
TGACTCATCAAATTATCCAATTATTAAC TACTAGACAAAAAGTATTTTAAATCAGTTTCTCT
GTTTATGCTATAGGAAGCTGAGATAATAAGGTA AATATGTATCATATAGATATACTATGT
TTTTCTATGTGAAATAGTTCTGTGCAAAAATAGTATTGCAGATATTGGAAAGTAATTGGTTT
CTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTCCTTTGAAACTAGTCC
CCTACCACTCGTGAATGAGCTCAATTACAGAAAGTGGAACATAGAAGAAATGAAGGGGACAGA
ATATCAAAACAGTGAAAAGGGAATGATAAGATGTATTTTGAATGAACTGTTTTTCTGTAGAC
TAGCTGAGAAATGTTGACATAAAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACTTAGACTTCTGTCTGCTAAATCTGTTCTT
TTTCTAATATTTCTAAAAA AAAAAAAGGTTTACCTCCACAAATTGAAAAA AAAAAA
AAAAA AAAAAA AAAAAA AAAAAA AAAAAA

FIGURE 19

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCNTTEGSYYCMCVPGFRSSNQDRFITNDGTVCIEENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLEQVYRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTL
SNSTLTETFKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFDFSYNMKHIHPHMMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSPTMTNGSWSSEGCETYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IISLICLAICITFFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTCGAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCCAGCCAAGAACCCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCTCTCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACACCCGGCTGGGA
CAAGAAGCCGCCGCTGCTGCCCCGGGCCCCGGGAGGGGGCTGGGGCTGGGGCCGGAGGCCG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGCTTTGGGCACCTACCCGTGGGGCCCGTAAGGCGTACTATATAAGGCTGCCGGCCCGAG
CCGCCGCGCGTCCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCCGCAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCC**ATG**CGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCCGTGCGCATCCGTGCCGACGGCGTGTGGACTGCGCGCGGGGC
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGCAAGCGTGGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCCCTGCCCATGCTGCCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTTGAATCTGACATGTTCTCTTCGCCCTTGAGACCGACAGCATG
GACCCATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAG**TAACT**
GAGACCATGCCCGGCCTCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCTCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTAGAGTTTTCCTATGGCAGTGCCAGTTTCTAGCCAATGAGTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCGCGGGCCCCATTTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGCAGGCAGTAGTTTAAATTTCAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTTCCC
CTGAGGCCAGTTCTGTGATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGC
TTCCATCTCCAGCCCACAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCAGCACTTGGTTTTCCACATGATATTTATGAGTAATTTATTTTATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCAAATTATTTATGTATGTAAGTGAGGTTTG
TTTTGTATATTTAAATGGAGTTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALLRTVAIKGVHVSRYLCMGADGKMQLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCTCCAGATTAGAGTGGAAGAAACTGGGTCGGAGTGCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGCGTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA
CAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACTGGAACT
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC
TGTGATATCGCAGGTGTCTTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTCCAGAAGAGTAATTTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGAAGG
CCGCGCGGGCGGATCACGAGGTGAGGATTC**TAG**ACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTGCACTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTIVSSRLE
WKKLGRSVSFVYYQQTLLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQONLEED
TVTLEVLVAPAVPSCVEPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTLLQFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNIISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGACCTGGCAT
CATGCTGCTATTCTTGCAAACTACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCTATGACCACTCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTGGACAATG
CAATTGTGGCACTGGCACTTATTTCACTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCA
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGACTG
TGGAATCCTTAAGGGCCCATTTACATTTCTGAAGAAGAAAGCTAAGATGAAGGCATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTCAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCCTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAG
ACTTTCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAAATTTATCTTCACTCAACCAAT
ATTAATGTAAAAAGATGCCCTCAGCTCCTTCTGTGTACCTAGAGGAAAAACAACCTTACTGA
ACTGCCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAACTCTATATTAATCACAAC
TGCTTTCTACAATTTCACTGGAGCCTTTATGGCCTACATAATCTTCTTCGACTTCATCTC
AATTCAAAATAGATTGCAGATCAACAGTAAAGTGGTTGATGCTCTTCCAAATCTAGAGAT
TCTGATGATTGGGGAAAATCCAATATCAGAATCAAAGACATGAACCTTAAGCCTCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCAGAGAAATACCAGATAACGCCTTGGTT
GGACTGGAAAACTTAGAAGCATCTCTTTTACGATAACAGGCTTATTAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAAATCCTATTAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAATAATATGCCT
GAGCTGATTTCCATCGATAGTCTTGTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACAAACCTTAGATTGCTTTACATTCACCCCAATGCATTTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATTGAGCTCTGTG
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTCTGAGAGCCAGATTCACTGTTTTGCGTGGACC
CACCTGAATTCGAAGTCAAGATGTTTCGGCAAGTGCATTTCAAGGACATGATGGAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTTTCCTTAATACCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAAATGGCGTAACCTCCCAAAGAGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTAATAAGAGATATTCAAGCCAATTCAGTTTTGGTGTCTTGGAAGCA
AGTTCTAAAATCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATCTCA
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAAATTTGTATTGATATTCCACCATTCTACGAAAAACAGAAAAAA
TGTGTAAATGTCAACCAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAAATAATAC
CACAACCTTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATGGTGTGATATGTCTTATCA
GTGCCCTCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
AGAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCACCAAGGAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPRIHVLLGLAITTLVQAVDKKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKMPQLLSVYLE
ENKLTPEKCLSELNQLQELYINHNLSTISPGAFI GLHNLLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLNLESISFYDNRL
IKVPHVALQKVNVNLFDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGHTIESLPNLKEISIHSPNIRC
DCVIRWMNMNKTNIREFMEPDSLFCVD PPEFQGNVRQVHFRDMMEICPLIAPESFPSPNLNV
EAGSYVSFHCRTAEPPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTA
FVKTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLGIIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCAATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCTCTACAAAGTTTGTTCCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCCAAAATCAGGAG
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTTCATTGAGAAAGAAAGAAA
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTGAA
ACTTTGTATTTTCAGTTTTTTTTGAATTATGCCACTGCTGAACTTTTAAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAAGCTTAACCTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTC SNANLKEIPRDL
PPETVLLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGV AETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVI CKTSVLDEHAGRPF
LAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKS LPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCTGCTGGCAGCCCATCCTCCTGCTGGTGTCT
GGGCTCAGTGCTGTGAGGCTCGGCCACGGGCTGCCCGCCCCGTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGTGTGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGTCAACAGAGAACATCGTGAGCGCCGTGGAGCCCGCG
CGTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCTGAAGCTCATC
CCGTAGGCGTCTTCACTGGCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACCAAGAT
CGTTATCCTACTGGACTACATGTTTTAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAAC
TGCCTCTACGGCCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCTACACCCCATCA
GCACCATGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCGAGAGATCCAGCTGGTGGGC
GGGCGACTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGCTCTTGGAACACAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG
CGCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACTGCCGCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
GTGTGCCGGGCGATGGCGACCCGCGCCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT
GGTCTCAGCCAAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCAGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGTCATCGCGGCCAACGCGGGCGGCAACGAC
TCCATGCCCGCCACCTGCATGTGCGCAGCTACTCGCCGACTGGCCCATCAGCCCAACAA
GACCTTCGCTTTTCATCTCCAACACGCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTGTCTCTCTTCTGCCTGGTGTCTGTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGTATGTGCCCCGAAAGTCGACGACGAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGCGAGGACCCCG
GGCGGCCGGGACGGGGAAGGGGCTGGTGCACCTGCTCACTCTCCAGTCTTCCACCTC
CTCCCTACCCTTCTACACAGTCTCTCTTCTCCCTCCCGCTCCCGTCCCTGCTGCCCGCG
CCAGCCCTCACCACCTGCCCTCTTCTACCAGGACCTCAGAAGCCAGACCTGGGGACCCCA
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT
TATGAAAACCTTGAAATAATAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGVSRMSPDLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLELELNENIVSAVEPGAFNNLFLNRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLSLEQLTLEKCNLTSIPTREALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLEH
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSHVGNLETLILDNPLA
CDCRLLWVFRRRWRLNFNRRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIILWLSPRKHLVSAKSNGRLTVPDGTLEVRYAQVQDNGTYL
CIAANAGGNDSPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTTCGGTCAAC
ATCGTAGTCCACCCCCTCCCATCCCCAGCCCCGGGGATTACAGGCTCGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATAGGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC
TGTTTCGCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCCTGGTGGTCAAGTGCCAAGTGAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTGAGTGGTTACCTCTACGCCCCAGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAAGTGCCAAGTCCCTCGTCACTGTGCTAGGAATCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTGAGTCTTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACTTCACTGTGAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCACCTCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGGCGCCTGCCCACTTCTGTC
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAA
CCGACAGGGCCGCCCTCCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGAATGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCGGTGGCTTCTCTGCATTTGGGTTATTATTATTTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

FIGURE 32

MGAPAAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSSSLQW
SNPAQQTLYFGEKRALRDNRILQVLTSTPHELSSISISNVALADEGEYTCISFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHLCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIIMLIFLGHYLIIRHKGYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCAACCCCTTTCTCTCTCTCTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCTCTTTGTTTTGCGCTGGAACGTTACAGGGGACGTTTGCAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTTCACTGCCCCGACTTCCAGTTTTTACCATTATTTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTGCGTAACCTTTTATAATGCGGTTAGTTTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTTCCGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTTATACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAACAATTCCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAAGGCTGTGCTCCAAACGGAGGTACAAAGATCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA
GTTTACCCTGCCCTGGGGGCTGCGAGCTGCGACCACATCCCAGGGTCCGGTTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTTCTGTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAAACAACATTTCAAG
AACCCTTTTGGACCTCGAGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTTCTCAACAACAACCTG
CTGAGGTCCCTGCCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
TAGAAAAGGATTTATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGACGCACTCC
AACTCTTACCTAGACACCAGCAGGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGTCTGTGGT
GTTTGTCACTCCGCTTCAACGTGGTGGCATGCTCGTGTATTATCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCTTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCCTTCCCCACCGCAGGCAACCCCGGGGCTGGAGGGCGGTGTACCCAAATCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAATACTGTGAGCTCGCACAAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCACAGCACTCTGCTGGAAG
AACTGACAGTGCCTCGCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
GTGAAATAAGTAACTTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKISFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLLEVLILNDNLISTLPANVPQYVPTIHLDLRG
NRLKTLPEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNQGEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANS LCPGGCSCDHI PGSG LKMNCNNRNVS SLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLDDLRLWLYMDSNY
LDTLSREKFAGLQNLLEYLNVEYNAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLL VFTSAFTVVGMLVFILNRKRKRKRDRANDSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTGTACCCGGCGCCAGCTGTGTTCTGACCCAGAAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGCGCCTAAGGGAAACTGTTGGC
CGCTGGGCCCCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGAACCGGGTTGGGGAAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCTCGAGCGGGACAGATCCAAAGTTGGGAGCAGCTCTGCGTGCGGGGCCCTCAG
AGAATGAGGCCGGCGTTTCGCCCTGTGCTCTCTGCGAGGCGCTCTGGCCCGGGCCGGGCGG
CGCGGAACACCCCACTGCGGACCGTGTGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCTGCGGGCAGGCCCAGG
GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
GCACCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGCGGTCTC
GAAAGCGACACGCTGCACTGGGTGGAGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
GGGAGGTACCTCCGTGTGCAAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTTGCCCTGCGAAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGGGTGCCACAGGCGCCCGCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTCACTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCAGATGTCTACCCCTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCCAAGTTTAATTTACGACTTCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTACGAAAGCCCCCTTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACATGGGGTGAAAGTCGGGGACTGTGATCTCGGGACAGAG
CAGAGGGTGCCCTGTGCGGAGTCCCCTCTGGCTCTAGTGATGCAATAGGGAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTAC
TTGTGTAACTGACAATTTCTGCAGAAATCCCCCTTCCCTCTAAATTCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCTTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTCTTATGTTTATTCGGAGAA
TTTGGAAGAAGTGATTGAACTTTTCAAGACATTGGAACAAATAGAACACAATATAATTTACA
TTAAAAAATAATTTCTACCAAATGGAAGGAAATGTTCTATGTTGTTTACGGCTAGGAGTAT
ATTGGTTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQ RSTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCTIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDG RSCVTSSEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDEPEAALGSSSAHCTNNGVKVGDCLDRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCCGCCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGGGGCAGCCGA
GCGCCGCTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCGCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA
GGGGCGGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGTTTTCTCGAGTGTACCCTCCAAATAGCAAATGTACTTTGGAAAAATCA
CAGTTCGCCAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCTAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGGATTACCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAGTTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAAATTGAAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA
AACTGCGCTACAACACAGAGCTGTACCACCACATTCCCTGTAACCAAGGTTTAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
CAGCCACAGTCTCGATCATCAACATCTACAAAGAGGCAAAATTTGGCGATTACAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTGCTCTGCAAGCAGTGCCCTCTCCTCAGAAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAATAAGCAATG
TTAACAGTGAACTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCCCTGCTGTGAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTATTATACATCTCTGTAAAGGAT
ATTTTAGAATTGAGTTGTGAAGATGTCAAAAAAAGATTTAGAAGTGCAATATTTATAGT
GTTATTGTTTTACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCCTTTTCTA
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAAAAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFVTCGGILTGESGFIGSEGFPVYPNSKCTWK
ITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLDRPSGSFKTFPNWPD RDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLP TTTEQPVT TTFPVITGLKPTVALCQQKCRRTGTLEGN
YCSD FVLAGTVITITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGACTGGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCCGCCTGCTGGAGCT
GAGTGAGGAGCTGTTGGAGAGCTGGTGGTTTCAACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGACGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAAGTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTAAAGAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAAACCCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATTA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGTAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTACCCACATCCCCACCCCCATTGCCACTTATTATTATCTCAGGAAATAAGA
AAGGTCTTGAAAGTTAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKCCPAGTFGSPCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEARNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDDIDE
CGTEGANCGADQFCVNTESGYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVLVQLQQMFFG
IIICALATLAAKGLVFTAFIFGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCCCCCTGGACAGGGCCGACATGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGAAAGAGGTTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
AGCCGGTCCCCAAGCCCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTGCGTGCAGAGG
GAGCATCTGGGCCCCTGGCGTCCGCGCCCCACAAGCTGGTCCGCTTTGCCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTCCAGGGTACCAGGAGAGCTG
GCGATGACTGAACCTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTGTCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCAATTGTTTACTTGTCTGTAC
TGGATCTGGGCTAAAGTCTCCACCACCACCTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAACATGAATAAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPR SARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLG DYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGT CRQPPEALAFKWP
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGAATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTCTTCTCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACGACTCGTTTGTCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCTCCTCTGCCACCATTTGGGAACCGGG
CAGTGCTGACATGCTCAGAAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCTATGTCCT
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCTGTGACCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTTCATCGTGGCAGCCGTCCTTGTAAACCCTGATTCTCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCCTGGTGTGAGCCTGGTCCGGCTCACCGCCTATCATCTGCATTGTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTC
TACACCCCAAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTGAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACTTGTTTAAA
GTGTTTATTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGCAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCCGGAGTTCCGGGATCAGCCTGACCA
ACATGGAGAAACCTTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAAACAAGAGCAAAAACCTCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLS CAYSGFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGT YTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGI VMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQP SARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCCTGGCGCTGCTGCTGCTCGGCCCTCGGACTAGGCCCT
GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGAGGCCCCAGCTCAG
GCTCGTGCACCCACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAAC TGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCC GACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCC GGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCCTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGT CAGAACAGAAGAC
CTCGCTGCCCTTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPTKFOCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGELRCTLSDDCIPLTWRC DGHPCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGTTTTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCAGTGCCTCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTAATGGAACCTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTGATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGCATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGTGGGGACTGTGATCTCCTATCGCTGCTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTGCTCT
GCCACCCGCGGCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCTCCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTGCTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAGGCCCACCTTCCCCCAGGGGGCTCCCCGGAG
TTCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCTGCTTCGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACAGCCCAGGCATCCATCATGCCCCACTGGGT
GTTGTTCTTAAGAAATTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTTAAAGNAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTGCGTGGCCTAGAGA
TGCTGCTGCCCGGTTGCAGTTGTGCGGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
AAGTTCAATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAATTTAGGAACTGGTATGTGGATGAGCCGTCCTGCGGCACGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCCTACATGTTCCAGTGGAATGATGA
CCGGTGCAACATGAAGAACAAATTTTCATTTGCAAATATTCTGATGAGAAACAGCAGTTCCTT
CTAGAGAAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTTCATTCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTTTCTTGCTCTATACAG
CAGCATATTTATCATACAGACAGAAAATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQK LIEKFIENLLPSD GDFWIGLRRREEKQSNSTACQDL
YAWTDGSI SQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWDDRCNMKNNFICKY
SDEKPAVPSREAEGETELTTPVLPEETQEEDAKKTFKESREAA LNLAYILIPSIPLLLLLLV
VTTVVCWVWICRKRKREQDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETR PDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGACTTGCGGGCGCCCGCTGAGCCCCGCGCCCCGAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCATAACACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCTGTGTTTCGACACGGGGCTCGGAGTCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCACTATTAGAGGTCCACCCCAAACCTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCT
TTTACCAACCTTCAACCCACAGGAGGTCTTTATTCTGTTCCACTAACATTTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGTCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTGCCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTGAGTTTATACCTTAAGCCCAGAAAAATACCATGCACCTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTTAACTGATTTATAAAGCAGGATGTGTTGATT
TTAAATAAAGTGCCTTTATACAATG

FIGURE 52

MITGVFMSRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSNIFRNLESTRCLLAGLFCQCKE
GPIIHTDEADSEVLYPNYQSCWSLRQTRGRRTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHNLPSCPMLKRFARMIEQRAVDTSLYIILPKEDRESLQMAVGPFLLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPDLMFLNAMS VYTLSPPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGACAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTACAGCTCATCACCTTCACCTGCGCTTGGTCAATGGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTCACACAGACCTGGATTCTAGCGTCTCCATCTGGAGTGGCGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAAGACGTGGCTGTGTTGTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTGACGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCATCTGCGTGTAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGAACTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACCGAATTTTAAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEADAGASC
ENPESSEFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVTCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWGSVCDNNGEKEDQVVKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGPHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTTCATCACCTCCACAGCCATCCTGCCCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCGGCTGCTGCAGTGGGTGCGCGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATGTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGTCTCACAAAGTGGG
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAAAGTAAAAAAAAAAAAAAAAAGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCCGRNGGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCCTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTCTAA
GAGGAGAAAATCAGTCACCGCGGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGTCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
GGTAGACTGCAGCAACCAGAGAAGATATTTACAGCTCTGCAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTTCCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATACTGGAGTCAAAACAACATG
TCTGTGTCTTAATTTCTGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCTCTA
ATAGTGCCAGAATTTTAAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTGTAGGCTTTGGCAGTCTTCATTTACTACCACTGTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGTATTGCACTTAAATTTGT
ATAATTTGTGTTTCTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTACAATGAATATCATGAACCTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTTCCAATGCCAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACCGTGTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AAA
AAA

FIGURE 58

MKFLLDIILLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKKGLGAKVHTFVVDSCNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLDLAAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGCTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGA
AGAGTTTATGCCGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTCTGGTTC
TCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGCCCTTATGTTGTCAACAAGTAACATGA
CCTTGCGTGACAGAGACTTCCCCTGGAACCAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTTACAGTGCACCTAATTAGTTTTTCCAGATATTTCTGAATATAAAAAATA
ATGACTTTTATGTCACTGGGAGTCTTATGCAGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTTGAGGCCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTTAAATGATGGAACCTATAGTTGAAAAGTACTTGCAGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGTATGGC
ATGGACTGGAAGGATCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATT
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGAAAAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAAGAGAACAT
CAGAGGTTTTTCATGTCTGAAAGAAAATCGTAAAAACAGAAAATGTATAGGAATAAAAAAA
TTATCTTTTATATCTGCAAGATTTTTTTCATCAATAAAAAATTATCCTTGAACAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTTGAATAGGAAGTTTTTAATTTCTTCTAAGAGTAAGTGAAGAGTGCAAGT
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAAATTATATATAAAAGTAAAAA

CCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC

FIGURE 60

MVGAMWKVIVSLVLLMPGPGCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPFPGGLNMKSYAGFLT VNKTYNSNLFWFPPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWT TTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALI QF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHS LNPNVREV KINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNV TG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVL IYNGQLDIIVAAALTERSLMGMDWKG SQEYKKA EKKVWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT
TTTTCCCTTTCCCTAACAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAGG
TCTAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTTAACTCTCTGGGAGATGAAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAAATAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGACCCTGGGTC
AGGCCAGCCTCTTTGCTCCTCCCGAAATTATTTTGGTCTGACCCTCTGCCTTGTGTTTT
GCAGAAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGTGGCCCCCAGCAGCCGGC
ATGCCTCAGTTACAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTAACCCG
CCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAAACCGCCTGCTGGCCTGTGGGAGCCTTACCAGGGGGTCTGCA
AGCTGTGCGGGCTGGATGACCTCTTCATCCTGGTGAGCCATCCCAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTTGTGCCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCAGCCCTGTCCA
GCCGGAAGCTGCCCCGAGACCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCCACCTTGACAT
CTTCTACATCTACGGCTTTGCTAGTGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCTGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCTGCCCCCTTCCGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAGGGCAGAAG
CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCTGCAGTCTGTCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTT
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAGAGTCCCTCTTGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCACTTTATTTTCTTGGGGAACAAGGTTGAATGGGGAGGTAAGAAGGGGTTAATTTGTG
ACTTAGCTTTAGCTACTTCTCCTCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCAACTTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPNGYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGSL
YQGVCKLLRLDDLFIIVPEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLRDPFESSAMLDDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSAFCAPPIRAINLQIKERLQSCYQGEEN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLLKKVRVYEFRCNSAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGCAGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCGATGACCA
 CGTGGAGCCTTCCGCGGAGGCGCGGCCGCGACGCTGGGACTCCTGCTGCTGGTCTCTTGGGCTTCCTGGTGTCTCC
 GCAGGCTGGACTGGAGCAACCTTGGTCCCTCTGCGGCTCGGCATCGACAGCTCAGGCAAGGCCATGGA
 ACTTCATGCTGGAGGATTCCACCTTCTGATCTTCGGGGCTCCATCCACTATTTCGCTGTGCCAGGGAGTACT
 GGAGGGACCGCTGCTGAAGATGAAGGCTGTGGCTTGAACACCTCACCACCTATGTTCCGTGGAACTGTCATG
 AGCCAGAAAGAGGCAAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCTGCTGATGGCCCGCAGAGATCG
 GGCTGTGGGTGATTCTGCTCAGGCCCCATCATCTGCAGTGAGATGGACCTCGGGGGCTTGGCCAGCTGGCTAC
 TCCAAGACCTTGGCATGAGGCTGAGGACAACTTACAAGGGCTTACCAGAGCTGGGGACCTTTATTTTGACCACC
 TGATGTCCAGGGTGGTGGCACTCCAGTACAAGCTGGGGGACCTATCATTTGCCCTGCAGGTGGAGAATGAATATG
 TGCTCTATAATAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTTGGGAACGTC
 TCTGACTTCAGACAACAAGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT
 CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGCTCAGGGGACTCAGCCCAAGATGGTGTGAGT
 ACTGGACGGGTGTGTTGACTCTGTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTGGAAAACCGTGT
 CTGCCATTGTGGACGCGGCTCCTCCATCAACCTTACATGTTCCAGGGAGGCACCACTTTGGCTTCATGAATG
 GAGCCATGCACTTCCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
 ATTACAGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
 ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACTGTCTCTGTGGGACGCCCTCAAGTACC
 TGGGGGAGCCAAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTT
 TCGGGTACATTCTCTATGAGACAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
 TGTTTGTGAACAGATATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
 ACACCGTGTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG
 GCTTAATTTGAAATCTCTATCTGAATGATTCAACCCTGAAAACTTCAGAATCTATAGCTTGGATATGAAGAAGA
 GCTTCTTTTCCAGAGTTCCGCTGGACAATGNGNTCCCTCCAGAAACACCCACATTACCTGCTTTCTTCTTGG
 GTAGCTTGTCCATCAGCTCCACGCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA
 TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAGAAGCGCTTACCTCCAGGTCCTTGGTTGA
 GCAGCGGAATCAACCAGGTCATCGTTTTTGGAGGAGACGATGGCGGGCCCTGCATTACAGTTTCCAGGAAACCCCTC
 ACCTGGGCAGGAACCAAGTACATTAAAGTGAAGCGGTGGCAACCCCTCCTGCTGTGTCAGTGGGAGACTGCCGCTC
 CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG
 ACTGGGGGCTACAGTCTGCCCCGTCTCAGCTCAAAACCTAAGCCTCGAGGGAAAGGTGGGATGGCTCTGGGCC
 TGGCTTTGTTGATGATGGCTTTTCTACAGCCCTGCTCTTGTGCCGAGGCTGTGCGGGTGTCTCTAGGGTGGGAGC
 AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGACCGGACGTACAGGCC
 TGCAGCATCTGTGACTCAGGCGTGTCTTTTGTGTTTCTGGGAGGCTTGGCCACATCCCTCATTGGCCCCAT
 TTTATCCCCGAAATCCTGGGTGTGCACCACTGTAGAGGTTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
 CTTCCTTCAACCTTCTGAGCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCTT
 TCCCTTCCCACTCGCTGCTTCCCAAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCTGTGCTTCC
 CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
 CATCCAGGGAGGAGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC
 AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA
 GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAG
 ACAGAAGGCCAGCTCAGTGGCCCCGTCTCCACACCCCCACGCCCCAACAGCAGGGGCGAGAGCAGCCCTCCTTC
 GAAGTGTGTTCCAAGTCCGATTGTAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGTA
 GTTGCAGTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRRPARTLGLLLLVLVGLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDPSGNLDLEAFVIMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTAEVDLYFDHLSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELELLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLENVQGTQPKMVMEYWTGWFDSWGPHNILDSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGNGQSFGYIILE
TSITSSGILSGHVHDRGQVFVNTVSI GFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFG LDKWXS L PETPTLP AFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLP GPWLS SGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGGTCCC
AAGAAGCTGTCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGTTCGTTCTGTAGTGGATAGGGGTATGACCGGTTTTCTCCTAGACGGGGCCC
CGTTCCGCTATGTCTCTGGCAGCCTGCCTACTTTTCGGGTACCGCGGTGCTTTGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTTGCCGAGTGGACTCCTGGTCAAGGTCTTGCTGCCCAAGATATATC
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTGAGTGGAGAATGAATATGCTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTTCCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACCTGTAGATTTTGGCCCCAGCTGACAAACATGACCAAAATCTTTACCTTGCTT
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGTCTTTCGAGATGTATCAGCAAGT
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGGCCAT
TCATTCAATCTTGCCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATACCATTTTTGAAGCCAACACCATTTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCCCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG
AGACAAACTATTTTGAAGCGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCTGTGTAAGCCACCAATTTCTG
GGGCAACAACTCTTACCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCCTCCAGTTGCCAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAAATTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCCAAGTCTGGATCAATGGGTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTCTACGTGCCAAGATTCCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA
CATTTGTGGAAGTGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCATATC
CTCAATAGCACTAGTACTTTGTCACAGGACACATATCAATTCCCTTTCAGCTGATACACTGAG
TGCTCTGAACCAATGGAGTTAAGTGGGCATGGAAGGTAGCCGGGCATGGTGGCTCATGC
CTGTAATCCCAGCATTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGGCGTG
ATGGTGGGCACCTCTAATCCAGCTGATTGGGAGGCTGAGGGCAGGAGAAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLCLKMRWSGLNAIQFYVPWNYHEBPQGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGlyTTVDFGPADNMTKIF
TLLRKYEPhGPlVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMymFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMrdKLF LTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWYPQAPSGPTFYSKTFPILGSVGDTFlyL
PGWTKGQVWINGFNLGRYWKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCCTCTACACTCTCTTCTGGTTATTCCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAACTCAGGCAGCACATTTCAACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCAGTGATGTGGCTGAAATTCTGCCTGGGTGTATTGTCTCAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTACATAATGACGGCAC
TAAACTCTTGCTACTGAACAGCCTTAAGAAAATGATGAATGTGCTGAGCTGGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTTTCCAGCATTTAAAAAGCT
GACTTGTTTAAAAATTATGGCATAACAAAATTGTACTATTCTCTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAAC
CTTGGACCGCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTGTATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGTTCTTTTTAAATTGTTTGTAACTGGAT
GCTGCCGCTACTGAATGTTTACAAATGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIIICVYGFICLYTLFWLFRIPLKEYSFEKVRRESSFS DIPDVKNDF AFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISRNAQDKQELH LFM LSG
VPDAVFDLTDL DV LKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLSENKMGIGLESRLRELRLKILHVKS NLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAEELQNC ELERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRCLDVSYNNISMIP IEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLS QLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDHLFD TLP LEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

[illegible][illegible]

FIGURE 70

MELVRRMLPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKHPPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVIISKSYLEAFNSNGNQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQQLQIIIVKCEMGHNST
VEIIYITEDDDVIQSQUALGKYNTSMALFESNSFEKTILESPPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAPKFLRSMSSVYL
QCKVLCIDSSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFGHETHA
EETPNQPFNSVHLFSFMVLALNVVTATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTG
TGCTGCCGCCGCCGCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCTGGTTTGAACAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTTTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTTAATGCCAACCACTGGGCGAGATATTTTTCAGGC
CTCTGGTGGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCGTGGAACCTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACCTGACCTGCGTTTTGGACTGTACTATTTCCCTTTTGA
ATGGTTTCATCCGCTCTTCTTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACCTGCATGACAATAGACAACTGTCTTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTGATGAATATTGGGGCCACACTAGATGGCACCATTTCTGTAGTTTGTGAG
GAGCGACTGAGGCAAGTGGGGTCTTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTACCCCGAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTCTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTTCCAGCCCTTTCCCTTTTTCCCACTA
AATTTTTCTTAAATTACCCATGTAAACATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC
TCTTCAACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAAATTTTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTGTGGCCAAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAACATAGAGAAG
GTACAGTAAAAATACTGTAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAA
GTTTTTCTTTCTTCAATTATAAATAACATAAGTGTAAGTGAACCTTACAAACGTTTTAATT
TTTAAACCTTTTTGGCTCTTTGTAAATAACACTTAGCTTAAACATAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPWTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSTKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAINRNTDLRFGLYISLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHGPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCACG**ATGGC**CAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTTTTGGCTGCAGAAAGACT
TTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACAGC
AGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTTCGTGGTCACTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
ACTTGGACTAACTCGTGCAATTCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTTGATTGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTTGTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC
TATGTCAAAGGATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACCTACCGTCGATGCCTGGAA
GCTGAAGTTT**TAG**ATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCC
TTACCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCCCTT
GGTTCTTAAGTGAATCAGCTCAGGACTGCCATTGGAATGAGAGTGACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAAGCTCAGAC
CCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTA
AGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAAATTGAG
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGACTGTAAACACAGACAGGCTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTAACCTCTGTAAT
TGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTCAT
GTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTTATTTTGGCTGAGACTAATCTT
ATTCATTTTCTCTAATATGGCAACCATATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTTGTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCATA
GCCCTCCTTTTCCAACAAGGAGGACTGAGAGATGCAGAAATTTTGTGACAAAAAATTAA
AGCATTTAGAAAACTT

FIGURE 74

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFNTKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGCGCGTCTTGGCACCTCTAATTGCTCTCGTGTATTGCGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTACTCGTGAGGAA
ACTGCCGCGGCTCTGCCACGGTCTGCCACCCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCATAGTGTTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCGTATCTGTTCACAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
TGGGGAAAAACAAGAAGGATAAA**TAA**GATCCTCACTTTGGCAGTGCTTCTCTCTCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTINATNATGTTTTCCTTTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTGTTCAGTGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC
AGCTATTCAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC
TAACCTCTGACATACTCCCCACACCAGTTGATGGCTTCCGTAATAAAAAAGATTGGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRNSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSPLTQQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

[illegible]

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVIVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRR LHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPFVVHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

[illegible][illegible]

FIGURE 80

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKFEDQLTPPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEFPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVWLPFAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTGCCAG
CCTGTCTGTGCTGCTTTTGGCGCCCCGCCCTCCCCGGGTGCGGGGTGACACCGGATCCTG
GGCTTGCCTCGATTGCGCCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTGCTCTCTCTCTGTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCT
GAGGAGGTGACGCGCGGGGCTCTCCCGACCTTGGCCTTGCCCGCATTCTCCCTCTCTCCAG
GTGTGAGCAGCCTATCAGTCAACCATGTCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGCCCCGCGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACCTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTTACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAGAAAACCTGG
CAATAAAGATTGTAAAGCAGACATTGCAATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTAAATTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCACATGTGGGCCTTGTTCAGCCAGTGAACATCCAAAATAGAATTTTACTTGAA
AAACTTTACATCAGCCAAAGATGTTTGTGGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATTCGAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTTCAGGATGTACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC
ATGCTTGAATTTGTTTCCAACATAGCCAAAGACTTTTGAATCTCGGACATTGGTGGCCAAGAT
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACC
AAGAGAATGTCCTAGCTGTATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTTCTTCACTGTGTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTACAGATGGGCAGTCTTATGATGATGTCCAAGGCCTTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTTCTGTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCACAAGAGAGTTTCACAGGAT
AGAACCAATTGTTTCTGATGTATCAGAGGCATTGTAGAGATTTCTTAGAATCCAGCAAT
AATGTGTAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTTGTATT
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACATATTAAGTATGTCAAC
AGCCATTTAGGCAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACCTCAGGAAAGAGGA
GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAGAATCTGATACTTAGACCAAAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFVSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCHEQMMCSKTCYNSVNI AFLI
DGSSSVGDSNFRMLLEFVSNI AKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACC GCGCGCTCCGCGATCTGCACCCGAGGCC
GGCGGCTCCCGGCGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATG CAGCGGCTTGGGGCCACCCCTGCTGTGCCTGC
TGCTGGCGGCGGCGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCCGGCCCGGCTCTCAGCTACCCG CAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACTGATGGAGGACACGCAGCACA AATTGCCGAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGA AGTGAACCTGGCAAACCTTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTG GAAATAATACCATCCATGTGCAACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACA AATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGCGAGAAGGAGCCACG AGTGCATCATCGACGAGGACTGTGGGCCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTAC ACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGGAG ACCAGCTGTGTCTCTGGGGTCACTGCACCAAAA
TGGCCACCGGGGCGAGCAATGGGACCATCTG TGACAACAGAGGGACTGCCAGCCGGGGCTG
TGCTGTGCCCTTCCAGAGAGGCTGCTGTTCC CTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTTTGCCATGACCCCGCCAGCCGGCTCTG GACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTG GCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGG AGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGC AGCTTCATGGAGGAGGTGCCCGCAGGACTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGAT GGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT
GCACTGCTGGGAGGGGAAGAGATTAGATCTG GACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCGAGGTGTGTGCTT TAGGCGTGGGCTGACCAGGCTTCTTCCTACA
TCTTCTTCCAGTAAGTTTCCCCTCTGGCTTG ACAGCATGAGGTGTTGTGCATTTGTTCCAGC
TCCCCCAGGCTGTTTCTCCAGGCTTCACAGT CTGGTGCTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATT ATTTGGCTGCTTTGCCCTTACCAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTG TTTGAGGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTTTTGGGGA AATGTGGAGAAGAGTGCCCTGCTTTGCAAAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTTCCAC GCAGTTCCTTCCATGGGCATAGGTAAGCTG
TGCTTTCAGCTGTTGCAGATGAAATGTTCTG TTCAACCTGCATTACATGTGTTTTATTCTCC
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCC AGGCGAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCAGCAGCCTGGGGAGGGGGTCA TTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTC ACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTC CACTACCCACACCAGCCTTGGTGCCAGCCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATT TTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACTAATTCACATCCCTCTAAAAGTAA AACTACTGTTAGGAACAGCAGTGTTCTCAC
AGTGTGGGGCAGCCGCTCTTAATGAAGACAATG ATATTGACACTGCCCTCTTTGGCAGT
TGCAATTAGTAACTTTGAAAGGTATATGACTG AGCGTAGCATACAGGTTAACTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAA ATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAAAT CAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACG CCACTCCACAAATGATGTTTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCATCCAGAGT TCTTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTTGAGTTTTTAAATTTATG TATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAA AAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYQEATLNEMFREVEELMEDTQ
HKLRSAVEEMEABEAAAASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQQRMLCTRDSCECG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCACAFQRGLLPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

[illegible]

AGGATAGGCTTGGGAGGAAGAGGCTAAGAAAGGTTTAGAGAACCTTACCTCACTCTCTCTGGGGCAGAGAAGGACTCTG
 AAGTAAACAATAATTTACGGCCCTTCACTCTCTCTCCCTCCAAACACATGTGTCATGTACACACATACATAC
 CACACATACACCTTCTCTCTCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC
 TAAAGCCTTAAGGACAGGCTTGCCCATTACCTTCGACGCTCTCTTTGGTGTGTGAGTCAAAAATCACTGGGAGGGG
 CAGGACCGGTGTACTACACTGTATTCACGCAATTTTGGGAGAGCCAGGTGTAGACAGATCACTTGTAGGCTCAGGAG
 TCTGAGACCGACCTTGCGCAACATGTGAGAAACCCCATCTGTACTAAAAATACAAAATTAGGCACAGGATGTGGTC
 AGGTCGCTGTATCCCGACTATCTCAGGTGSGCTGAGCGGAGGAATCGTGTGAATCCAGGAGGCGGAGGATGTCACT
 CAGCTGAGGTGACACCGCTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCATAACAAACAAACACGGGAGG
 GGGTGATAGATCTGCTTCTGCAACCTCTTAACTCTGCACTCTCTCTCCAGGCGTCCCTTGAATGTGGGGCTCT
 CCAATCACTGAGCAGGCCAGCCCGCAGAGGAACAAGGAGAGAGGCAATATTGAGGAGGGCGAAGAGTGACGCCCGC
 GTGTGAATAGTACTGCCCTGGGAGGGTGGTTCTCTTGGGCCCTGCGAGGTTGCTGACCTTACCTCTGCAAAAACAC
 AAGACAGGAGCTCAGACCTCTCTGTGTATGTCCTGCTGCCCTGACGCTCAACCACTGAGGCTCTCTGCTGGCCCC
 ACTCTTGTGATGTTGGGTGCTGGTGCCACTGCCACTGTGCCGTGCTGCTCCCTGGCATGTTCCCTGCCCCCTCA
 GTGTGCTGACAGATCGGGCCCTGGTATACGCCCCGCTGTGCTCTACGGCAGGCTACCATCTGTGGACTGCAATGA
 CCTATTCTGACGGCAGTCCCCCGGCATCTCCCGCAGGCAACAGACCCTGTCTCTGACAGAACAGCAAGTGTG
 CCGTGTGGACAGCAGTGTAGCTGGGTCATCTGCGCAATCTGACAGAGCTGGAACCTGTCCCAAGACAGCTTCTTGGGA
 TCCCGCAGACTGTGATTTTCATGCTCCCTGCCAGCTGTCTGACAGCTGTCACTTAGAGGAGAACAGCTGACCCGGCT
 GGAGGACACAGCTTTGCGAGGGCTGGCCAGCTCAAGGAATCTTATCTCAACCAACCAACAGCTTACCGCATCGC
 CCCCAGGCGCTTTTCTGGCCTCAGCAATCTGTGTGGGCTGTGCACTCTCAACTCAACCTCTGAGGCCATGTGACAG
 CCGCTGTTTGAATGCTGCCAACCTTGGAGATACTCATGATTGGCGGCAACAGGCTAGATGTCCATCTGGACAT
 GAACTTCCGGCCCTGGCCCAACTCGCGTAGCTCTGTGTGATGACGAGCATGAACCTCGGGAGATCTCCGACTATGC
 CTGGAGGGGCTGCAAGAGCTGGAGAGCTCTCTCTTATGATCAACACAGCTGGCCGGGTGCCGAGCGGCCACT
 GGAACAGGTTGCCCGCTCAAGTTCTAGACTCTCAACAGAACCCGCTCTGACGGGGTAGGGCGGGGACTTTGTC
 CAACATGCTGACCTTTAAGGAGCTGGGACTGAAACATGTAGGAGAGCTGTGTTCTCATCAGCAAGTTTGTCCCTGGT
 GAACTCTCCCGAGTGAACAGCTGGACATCAACCAATCAACCAACCGGCTGTCTCTTCAACCCCGCGCCTTCC
 CCACTGCCCGAGATGGAGACCTCATGCTCAACACAAAGCTCTCAGTGGCTGTCCACAGGACAGCGTGGAGTCT
 CCTGCCCAACCTGCAGGAGGTAGGCTCTCACGGCAACCCCATCGCTGTGACTGTGTATCTCCGCTGGCCCAATGC
 CACGGGCAACCGGTGTGCTGTTATCGACGAGAGCAATCCACCTGTGTGCGAGGCTCCGGAATCTCAGCGCTCTCC
 GGTCCGTGAGGTCGCTCTCGGAGAGATGACGCAACTGTTTGCCCTGTCTTCCCAAGAGCTTCCCCCAAG
 CTTCCAGGTAGCAGCTGGAGAGAGCATGTGCTGTGATTGCGGGCACTGGCCCAACCCGAGATCTACTGT
 GGTCACTCAGCTGGGCTTTCAGTCACTGCTGCCATCAGCAGGAGGATGACCGGTTGATCCCGTACCGGGACCT
 GGAGCTCGGAGGGTGACAGCAGGAGGAGCGGCTATACACCTGTGTGCGCCCAAGCTGGTGGGGGCTGACAC
 TAAGACGCTTAGTGTGTTTGGGCGGTGCTCTCTCCAGCGAGGAGGAGGAGGAGGACAGGAGGCTGGAGCTCCG
 GGTGACGAGGACCCACCCCTATCACATCTGCTATCTTTGGGTGACCCCAACCAAGTGTCCACCAACTCACT
 CTGTGCTCAGTGTGCTCTCCCTCGGGGCGAGGGGCGACAGCTCTGCGCCGCTGCTCTGGGGAACCCACAGTCA
 CAACATTACCCGCTCTCTCAGGCAACGGAGTATGCGGCTGCTGCGCAAGTGGCTTTCTGTGATGCCACACCA
 GTTCCATTTGTGATGGGCGAGAACAAAGAGGCCATCTTGTGACAGAGCTTAGGGAGATGTCTCTGGGCTCAT
 GTGCCTCTGGGCTCTCTGTCTCTCTCTGCGAGCTGGGTACGCGGCCACCTTGTGACAGGCGCAACCCAGGAA
 GGGTGTGGGTGGGAGCGGCGCTCTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGTGCCCTCTGTCTCGGGTGTG
 TCTGTCTCCCTCTGCTCCGCTGGAACTCAGGAGGGAGGCTCCCGAGATCTCAGAGGGGAGACATGTTGTGCC
 ACCATTGTCTCAAAATTTCTGAGAGCTCAGCCTGTGTTTACAGCTAGAGGAATCACTAGGACTCTTTTAAACAA
 AGAGAAGCAGTCTGGGCAAGTGCCTTCCGAGGAAGGGAACATGGACACAGCTGTCTGTAGGCTCTGGCAGCTGGGC
 CAGACAGATGTGGGCTTTGTGCGCTCTGGGGTGTCTTGTGACGCTTGAAAAAGTTGCCCTTACCTCTTCAAGGTCA
 CCTCTGCTGCCATTTCTGAGGAACATCTCAAGGAACAGGAGGACTTGTGCTAGAGACTCTCTGCTCTCCCATCTT
 CTTCTGCGCAGAGGCTCTGGGCTGTGCTTGGCTTCTCCCTACCTGTGCTCCCGGCTGACCCCTCTCTCTCT
 TCTTTCTGTACAGTCTCAGTGTGCTGTGCTTGTGTCCTCTGGGCAAGGGCTGAAGGAGGACATCTCACTTCACT
 CTTGAGGGGCTGCCCTCAATGTGGGAGTGACCCCGAGCAGATCTGAAGAGATATTTGGGAGAGGATGCCCGAGAA
 CGCTCATCTCAGAGGCTGGGCTGGCATCTCGAAGCTGACTTTTCTATAGGCAATTTGTGATCTTTGTGGAGAA
 ATGTGTCACTCCCCAACCCGATTCACTTTTCTCTGTTTTGTAAAAAATAAAATAAATAATTAACATAAA
 AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLQSNSTVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLSELSFYDNQ
LARVPRRALEQVPGCLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKDFALVNL
ELTKLDITNNPRLSFIHPRAFHHLPQMETMLNNNALSALHQQTVESLNLQEVGLHGNI
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPPFREMTHCLPLISPRSFP
VSGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVYPEGTLELRRVTAE
CVAQNVLVGADTKTVSVVVGRRLLQPRDEGQGLELRVQETHPYHILLSWVTPPNTV
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKE
ATSHRALGDRPGLIAIALALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGSAPS
VVRVVSAPLVLPWNPGRKLPRSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCGCTGTTTGGAGAAGGTGAAGAAGTTCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
 CTAC**ATG**CGGCGAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCTGCTACACCGGTCTACTACGTGCACAA
 CATCAAGTTTCGACGTGGACCTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACTTACCGCTGTGCCACCC
 CCTGGCCACACTCTTCAAGATCTTGGCGTCCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
 CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTTCGATCCGTGAGGAGAGCAGCTACAG
 CGACATCCCGGACGTCAAGAACGACTTCGCTTTCATGCTGCACCTCATTTGACCAATACGACCCGCTCTACTCCAA
 GCGCTTCGCCGCTCTTCTGTCCGAGGTGAGTGAGAACAGCTGCGGCAGCTGAACTTCAACAACAGAGTGGACGCT
 GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAAGCTGGAGCTTGACTTCATGCTCAGTGGCAT
 CCCTGACACTGTGTTTGACCTTGTGGAGCTGGAGTGCTTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCC
 CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACACACAGCGGCAAGATTGAAGCGCCTGCGCT
 GGCCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTTACCGACATCAAGGAGATCCCGCTGTGGATCTA
 TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACACCGCTACATCGTCATCGA
 CGGGCTGCGGGAGCTCAAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTAC
 AGATGTGGCGCTGCACCTGCAGAAAGCTGTCCATCAACAATGAGGGCAACCAAGCTCATCGTCTTCAACAGCCTCAA
 GAAGATGGCAACCTGACTGAGCTGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCCACTCCATCTTCAGCCT
 CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGACACT
 GCACCGCTCACTGCTTAAAGCTGTGGTACAACACATCGCTTACATCCCCATCCAGATCGGCAACCTCACCAA
 CCTGGAGCGCTCTACCTGAACCGCAAGAGATCGAGAAGATCCCCACCAAGCTCTTCTACTGCCCGAGCTGCG
 CTACCTGGACCTCAGGCAACAACCTGACCTTCTTCCCTGCGGACATCGGCTCTTGCAGAACCTCCAGAACCT
 AGCCATCAGCGGCAACCGGATCGAGAGCTCCCTCCGGAGCTCTTCAAGTGC CGGAAGCTGCGGGCTCTGCACCT
 GGGCAACAAGCTGCTCGAGTCACTGCCCTCCAGGCTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGG
 CAACCGGCTGGAGTGCCTGCTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGTGTGTGGAGGA
 GGACCTGTTCAACAACCTGCCACCGAGGTGAAGGAGCGGCTGTGGAGGGCTGAAGAAGGAGGGCT**TGA**GCGGAG
 GCGGCGCAGCAGCAAGCAGCAGGACCGCTGCCAGTCTTCAAGGCGGAGGGGCGAGGCTTAGCTTCTCCAG
 AACTCCCGGACAGCCAGGACAGCTCGCGCTGGGCGAGGAGCTGGGCGCGCTTGTGAGTCAGGCGAGAGCGAGA
 GGACAGTATCTGTGGGCTGGGCGCTTTTCTCCCTCTGAGACTCAGCTCCCCAGGGCAAGTCTTGTGTGGAGAG
 AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG
 CTGCCACAGAGGTCTGGGACCTCACTTTAGTTCTTGGTATTTATTTTCTCCATCTGCCACCTCCCTTCATCC
 AGATAACTTATACATTCCCAAGAAAGTTTCAGCCAGATGGAAGGTGTTTCAGGGAAGGTGGGCTGCTTTTCCCT
 TTGTCTTTATTTAGCGATGCCCGCGGGCTTTAAACCCCACTGGACTTCAGCAGAGTGGTCCGCGGCGAAGCAG
 CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCAGCGGAGAGCAGGCTTCCAGCTGGA
 AAGGCCAGGCTGGAGCTTGCTCTTCAGTTTGTGGCAGTTTATGTTTGTTTTGTTTTATTAACAA
 AAACAATTTTTTTTAAAAAAAGCTTTGAAATGGATGGTTTGGGTATTAAAAAGAAAAAAACTTAAAAAA
 AAAAGACACTAACCGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAGCAGCCAGAGCT
 TGAACGTGTTTCTTTCCCTGGGCGAGGGTGCAGGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT
 CTATTTGTTCTTGGGAGGGAGGTTTTTTGTGTTGTTTGTGGGTTTTTTTGGTGTCTTGTTTCTTCTCTCC
 ATGTGCTTGGCAGGCACTCATTTCTGTGGCTGTGCGGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
 ACTCGGTTGGCTAATCCCGGATGAACGGTGTCCATTGCACTCCCTCTCGTGCTGCCCTGCCCTCTCCA
 CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTTTCCCACTCTCGCGGCATGGGTGTGT
 CCAGTGCCACCGCTGGCTCCGCTGCTCCATCAGCCCTGTGCGCACCTGGTCTTTCATGAAGAGCAGACACTTA
 GAGGCTGCTCGGGAATGGGAGGTGCGCCCTGGGAGGGCAGGGCTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGC
 CTGGAGTGCAACAGCCAGTCGGCACCTGGTGGCTGAAGGCCAACTGCTTTAGATCACTCGGGTCCCCACCTT
 AGAAGGTTCCCGCTTAGATCAATCAGTGGACACTAAGGCAGTTTATAGAGTCTCTTGTCTTAATGATTATGT
 CCATCCGCTGTCCGCTCCATTTGTGTTTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
 CCTCTGACACCATGAAGCAAAATCCGTTACATGTGGTCTGAACCTGTAGACTCGGTACAGTATCAATAAA
 ATCTATAACAGAAAAA

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FIGURE 88

MRQTIKVIKFIILICYTVVYVHNKFDVDC TVDIESLTGYRTYRCAHPLATLTKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLS GIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPEL FQCRKLRLHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCCGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCAGGAAAACCCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTGCCATATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAG
AATTCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCCTTGGGTGATTCTCGGATCTCCCCGTGGATTTCGGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTTGAACAGAACACAGATGGGGTGAACTTCTATAACATCTTAACTAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGCCCTG
GGTGGCGAAACTGAAGTGCCAGAACTGCCTAAATTCACTGAGCTGAAGTGGAAGGCCCTGT
ACAGTGACCCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCTTACAAGAACCCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGCGACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELWGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSELEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKCLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLETSAFVKS YKNLAFYWILKAGHMVP
SDQGDMA LKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCAACTCGGGCGTTGGCCGTGGCA
GGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCAACCCCTCCAGGAAGTTCAGGTGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTTTGGTAATAAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCVSVLLSHRWALTAACHCFETYSDLSDPGWMVQFGQLTSMPSFWSLQAYYTRYFVSN
YLSPRYLGNSPYDIALVKLSAPVITYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
CTTTGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCCGAGCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCCTGGGCGGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT
GCCCTGAGACAGCAGAATGTGGAAGACTCTCGGAGCTGGTGCAGGCTGTGTCCGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTGTGAAGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCCT
GCATCTGGGGGTAACCCCTCTGTGATCCGTAAGCGATAACAACCTTGACCTCACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAAGCCTGTGCCAGTTCCCTGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCCGGGCCGGGCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGTCTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCTGTCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCGCTCGGGTCTCACCTGCTCTTCGCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
CCCCATGTCAACCAGTGGGAGGCACATCCTTCCAGGAACCTTTCCCTCATCAAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAAGCTGTTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGATAACGAAGTTCCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGTGGTCAGCAACA
GAGTGGCCATTTCCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTTTGGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAAG
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTCT
TGGATGAAGAGGTAGAGGGCCAGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAAACAGGC
TGGGGAACCAACTTCCAGCTTTGTCTGAAGACTCTACTCAACCCCTGACCCTTTCCTATC
AGGAGAGATGGCTTGTCCTTGCCTGAAGCTGGCAGTTCACTCCCTTATTTCTGCCCTGTTG
GAAGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCTGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACCTAGCATTTTGTGAATGCCTCTCCCTCCGC
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCAATCCCCAATTCAGTGAAGGAGACCTCTACTGTACCGTTTACTCT
TTCCTACCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGTCTTATG
GCCTTTCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTCTG
ACTACTCTTGTCTTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC
TCCATTTGTAGATTTTGTCTCTCTCAGTTTACTCATTTGTCCTCCCTGGAAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACCTCAA
TGTAACAAAA

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FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLNVADLVRPSPLTLHTVQKWL LAAGA QKCHSVITQDFTLCWL
SIRQAELLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQGRGRAGIEASLDVQYLSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGT SFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGLFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

[illegible]

CCCGCGCGCTCTCTCCGGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCGGGG
GGGCTGCTCGGCGCGGAACAGTGTCTGGC**CATGG**CAGGGATTCCAGGGCTCCTCTTCTTCTC
TTCTTTCTGCTCTGTGTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCTGTCTGTTTGGCCAGTCTACCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTATAAGGGAAT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTTCAGCATTTTTGGGAAGGACTTCCTGCTCAACTACCCTTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAAGCATGTCTCACAGCTGCCCACTGCA
TACACGATGGA AAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC
AAGTTTAAAGATGGTGGTGCAGGGGGCCAAACGACTCCACTTCAGCCATGCCCCGAGCAGATGAA
ATTTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGTCTAAGCAGCTGCCAGGGGGCAGAATTCATTCTC
TGTTTATGACAAATGACCGACCAAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAAGTGGGAGCGAAAAATTATTGGCATTTTTTTCAGG
GCACCACTGGGTGGACATGAATGGTTCCCAACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC
AAATTGTTTTTTGTCAATTGGCGTGACACGTGTGTGTGTGTGTGTGTGTGTAAGGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACTG
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA
AAAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG
CAAACCTTGATTTTTTATTTTCATCTGAACCTGTTTCAAAGATTTATATTAAATATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIIGIFSGHQVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCCTGCTCCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCTCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCCTCTGCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCTTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCGCGGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTTATCTCCAATTTCATAAATTATTTATT
CTCCAAAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLTTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCTGTATGCTTCTGCTGCCGCTACTGCTA
CTGCTGTTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC
AACAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACAGGCCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGGCTCTGCAGTCGTCCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTGAGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTGAGCTGTCCTCTGTGTCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCTGAGTGCCCTG
TGTAAGTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPITASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVLCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTPSSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGDPKPSV
SGLNSGPGHVWGPLLGLLLLPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

Parameter	Value	Unit
α	0.01	
β	0.01	
γ	0.01	
δ	0.01	
ϵ	0.01	
ζ	0.01	
η	0.01	
θ	0.01	
ι	0.01	
κ	0.01	
λ	0.01	
μ	0.01	
ν	0.01	
ξ	0.01	
\omicron	0.01	
π	0.01	
ρ	0.01	
σ	0.01	
τ	0.01	
υ	0.01	
ϕ	0.01	
χ	0.01	
ψ	0.01	
ω	0.01	
Ω	0.01	
Θ	0.01	
Φ	0.01	
Ψ	0.01	
Υ	0.01	
Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01	
Λ	0.01	
Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01	
Λ	0.01	
Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01	
Λ	0.01	
Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01	
Λ	0.01	
Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01	
Λ	0.01	
Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01	
Λ	0.01	
Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01	
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Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01	
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Δ	0.01	
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Π	0.01	
Γ	0.01	
Δ	0.01	
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Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01	
Λ	0.01	
Σ	0.01	
Π	0.01	
Γ	0.01	
Δ	0.01</	

TTAATCGAAGTCAGCGCTTTTTCATTTGGGAGAGCCCTTCAACAGAAATTCCGTGATCTTCCCAAGTATTGGTGGACGT
 ACTTCGTGTTTGTCCTCTCGCTTGCTTTTTCATTCATAGCAGCGCATTAAGTCAACAAGATTAATCTTCATCT
 CAAGGCAAGTTCATGAGCCAGTCTTCAAAGCCTTGAGAGAGTGAACCTGAACAACAATGAATTGGAGACCATTTCC
 AAATCTGGGACAGGTCTCGGCCAAATATTACCTTCTCTCTTGGCTGGAAACAGGATGTTGAAATATCTCCCTGA
 ACATCTGAAGAAGTTTTCAGTCCCTTGAACATTTTGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAATCGATT
 TCCAGCCCTTCAAGCTCAAAATATCTGTAATCTCAAACAGCAACCGAGTTCACATCAATGGACCTGGGTATTTGACA
 TTTGGCCAAACACAGCTCTTGTTGTTAAAGTGAACAGGAAACCGAATCTTCAGTATGCCACCAGGAATGTTAAACT
 GCGCCAACTGCTCAACATCTCGAAATTGAACCGAAACAGATTTAAATATGATAGTGACTGACATTCACAGGCTCTGG
 TGCTCTGAAGTCTCTGAAATGCAACAAATGGATGAACGAACCTTATGATGGTAGCTTTTGGGGGCTGAGCA
 CATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGC
 CAGGAACTTTCATCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCGGGATTTGCGCAAGATCCGAC
 TGAGCTGGACCTAACTTTCAATCACTTATCAAGTTTATGATGATTTCAAGCTTCTTGCCCTAAGCTTACATAAAT
 CTACGACATATGGGAAACAACAGATGCTGACTACATTTGCTGATTTGCTCTCGGGGGCTTTTCAGTTTAAAGACTTT
 GGATCTGAAGAAACAATAAATTTCTGGACTTTGAAGACATGAATGCTGTTCTTCTGGGCTGCACAACTGAG
 GCTAGCTATATCCAAAGGAATCGGATCGCTTCTATTACTAAACAAAGCCTTTCAGTGTTTGATGATTCATCGCA
 TGTAGACTCTGAGTGACAAAGCAATCATGTCTTATCAAGGCAATGCAATTTCAAAATGAAGAACTGCAACATTT
 GCATTTAAATACATCAAGCTTTTGTGCGATTGCGAGCTAAATGGCTCCCAAGTGGGTGGCGGAAACAACTT
 TCAGAGCTTTGTAAATGTCAGTTGTGCCATCTCCAGTCTCAAAAGGAAGAAGCTTTTGCCTGTAGCCGAGA
 TGCTTTTGTTGTGATGATTTTCCAAACCCAGATCACTCGTTCAGCCGAAACAACAGCTGCGGATAAAGGTTT
 CAATTTGAGTTTTCATCTGCTCAGCTGCCAGCAGCAAGTATTTCCCAATGACTTTTGCTTGGAAAGAACACATGA
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 CATCTCTTGCGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTTGTGATCTCCAATCATCTTTGGTTT
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 CCGAGCTGGGGCTATGCGACGCTTGAGTGTGCTGTGTGGGGCACCCAGCCCCAGATAGCTTGGCAAGGA
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 GGATGTGAAGATAGAGACAATGGGCTATACAGCTGCAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAATCG
 AACTCTGACTGCTCTGAGAAGAACCATCATTTTGGGCGCACTGTGGACGAACTGATCAACGAGGGAGAACAGC
 GCTTCTACGTGCTATGCTGAGGAGGAAGCCCTTCGGCTAACTGAACTGAACTGACCAAGATGATAGCCCTTTGGTGT
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 CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACATGACGGATGGGCACTTGGGGTGTGCTGATCATAGC
 CTGTGTTTGCTGTGTGGTGGGCACTGCTATCTGTGTGGTGTGATCATATACCAACAGGCGGAGGAATGAGA
 TTTGACGATTAACCAACAGCATGAGACCAACTTGCAGCAGATATTCCTAGTTATTGTGCTTCCAGGGAAGCTT
 AGCTGACAGCGAGATGGGTACGTGTTCTCAAGAAATGGAGCAACCAACAGTTTGTGCATCTTCAGGTGCTGTG
 ATTTTCTTACCACAAGATCAGTATGCTGGAGACTGTCATATGACAAATAGCATGGAGCTGATGTGAAGCTGC
 CAGATCTGTCTCTTTGTCGTTTGGGATCTCAGCGGCCATGATTTTGAAGGAAATGTGATGGCTCAGA
 TCCTTTTGAACATATACATACAGGTGTCAGCTCTGACCACCAAGACAGCTTTTATGGACCACTATGAGCCGCTTA
 CATAAAGAAAAAGAGTGCTACCCATGTTCTCATCTTCAGAGAAATCTCTGCGAACGGAGCTTCAGTAATATATG
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 TCTAAACAGTCTCTTTAGATTATTTAGTGCAAATCAGAGCAGCGCTGCTGGCTCGCATTAATCTTTTCATGG
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 AGAGCGCTTTTATTTGAAGCTCATCTTCCCCAGATCTGGACCTGGGTTCAGGAGAGAGTGGGAAGAAGAGC
 AGATTTTCAGGAAGAAATACATTTGTACTCTTTAAACAGACTTTAGAAACATCAGAGATCTCAAATTTTTCAGT
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 AAGAGAGAGAACTCTATGTTTTTTAAATGGAGTTATGAAATTTTAAAGGATAAAAAATGCTTTATTTATACAGAT
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 TTATATGCGAGATTTCTTTTATGAAAATGAGTATCAAGAACTTTTAAATATAACTCTCGCTTGTACCAATTT
 TTAATATAGAGGTACTCTATATATTTTGCATATATTTTAAATGTCTCAATTTGAA

FIGURE 102

MVDVLLLFSLCCLLFHISRDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSA
ITLLSLAGNRIVEILPEHLKEFQSLQSLTDLSSNNISELQTAFPALQLKYLYLNSNRVTSM
GYFDNLANTLLVLKLNRRIRISAI PPKMFKL PQLQHLELNRRKIKNV DGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTETITKGWLYGLLMLQBELHLSQNAINRISPD
FCQKLSLQDLTFNHLRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSLKTLDLKNE
ISWTIEMNGAFSGLDKLRRLILQGNRIRSIITTKAFTGLDALEHLDSLDAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLISFICSAASSSDSPMTFAWKKNELLHDAEMENYHLRAQG
GEVMEYTTILRLREVEFASGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSTAQ
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSVDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVVIIAIVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNLPAIDPSYLSSQGT
LAD RQDGYVSESGSHHQVFTSSGAGFFLPQHDSSTGCHIDNSSEADVEAATDLFLCPFLGSTG
P MYLKGNVYGSDPFETYHTGCSPPDRTVLMHDHYEPSYIKKKECYPCSHPSSESCERSFSN
ISW PSHVRKLNTSYSHNEGPGMKNLCLNKSSLDIFSANPEPASVASSNSFMGTGKALRRP
HLDA YSSFGQPSDCQPRAFYLKAHSSPDLDGSGSEEDGKERTDFQEEHNHICTFKQTL
ENYRTPNPFQS YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

[illegible]

AGGAGTGGAGGAAATTTGACCATGTAAAAGAGCAATTTTTTTTGGTGGTGGTGGCTGTGGGTGGCCTTGCAAAAATG
AAGGATGTCAGGACGCAGCTTTCTCTGGAAACGAAACGATGGTAATCACTGATTTGTGCAGAGGAGGAAGAAAC
GAAGCTTTTTCTTGTGAGCGCTGGATCTTAAACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAA
TAAACCCAGATTTAGACCCCGGGGGTTGGTGTGTTCTGCATATAATAATTTCTTAAGACGATGTTCTCCCTCC
CACCCCAAAAAAAGGATGTATGGAATAAGAAACGAGGATTTCAAAAGGAAAAAGATGTTCTATTTTTTCTC
TATAAAGAGGAAAGTTGAGCCCAAGGAGATATTTTGGAAATGAAAAGTTGGGGCTTTTTTTAGTAAAGTAAAGAACT
GGTGGTGGTGTGTTCTCTTTTGGAAATTTCCCAAGAGAGGAGGAAATTAATATACATCTCCGAAAGT
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAAACAGCAGAGCACAGTTGGA
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TTTTATTCTTTTGGTATCAAGATCATGCGTTTCTCTTTCTTTAAACCTCGGATTTCATCTGGAATGTGTCT
GTGATCAGTCTGAAATCAACTCTTTGTAATCCCAAGAGGACCAACAGGATTAATGTATGATTTGTAACAGACAT
GACCTTACATCCACAGCAGATAATGTAGTCTCTAGGTTTTCACAGGCGGTTTATGACCCCTGCTTGTGGTGTCT
GCTGGCTCTTCAACTCTTTGTGGTGGCTGGTCTGGTGGCGGCTCAGACCTGCGCTTCTGTGTGCTCCCTGCAGCAA
CCAGTTTCAGCAAGTGTATTTGTGTGGAAAACCTCGTGAGGTTCCGGATGGCATCTCCACCAACACACCGGCT
CTGAAACTCTCATGAGAACCAATTCAGATCATCAAAGTGAACAGCTTCAAGCATCTGAGGCATTTGAAACTCT
ACAGTTGAGTAGAGGACCAATTCAGAACCAATGAAATTTGGGGCTTTCAATGTTCTGGCGAACCCTCAACATCTGGA
ACTTTCTTGCAATCTGCTTTACTACCATCCCGAATGGAGCTTTGTGATCTTGTCTCAAGCTGAAGGAGCTCTGTT
GCGAAACAAACCCATTGAAAGCATCTCCTTTATGCTTTTAAACAAATTCCTTCTTTGGCCGACATGACTTTAGG
GGAATTTGAAAAGACTTTATACATCTTCAGAAGGTGCGCTTGAAGTCTGTCCAATCTGGAGTTATTGGAACCTGC
CATGTGCAAACTCTCGGAAATCCCTAACCTCACAACGCTCATAAAACTAGATAGCTGGATCTTTTGGGAATCA
TTTATCTGCCATCAGCGCTGGCTCTTTCTCAGGGTTTGATGCACCTCAAAAATCTGTGATGATGATCCGATCCGAT
TCAAGTGTAGAGCGGAATGCGTTTGACAACTCTCAGTCACTAGTGGAGATCAACCTGGGCACAAATTAATCAAC
ATTACTGCTCTCATGACTCTTTCATCTCCCTTGTCATCATAGAGCGGATCAATTTACATCAACACCCCTTGGAACTG
TAACCTGTGACATCTGTGGCTCAGCTGGTGGATAAAGACGCGCCCTCGAACACAGCTTGTGTGCGCGGT
TAACTCTCTCCCAATCTAAAGGGGAGGTACATTTGAGAGCTGCAGACGAATATCTTCATGCTGTATGCTCGGT
GATTTGTGGAGCCCGCTGCAGACCTCAATGTTCTCAAGGACATGGACCTGAGCTGAATTTGCGGGCCCTCCACAT
CTGCACTCTGTGATCTTTGGATATCTTCAAATGGAACTGATCATGACATGCGGGCTCAAAAGTGCAGATGCTGT
GCTCAGTATGTGATCTGTTAAATTTTCAAAATGTAATCTGTCAAGATACAGGCATGTACATGATGTATGTGGAGTAA
TTCGGTTGGGAATACCTGCTCTCAGCCACCTCGATGTTTCTGCAGCAACCACTACTCTTTCTTTCTTTCTT
AACCGTTCAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCACTCC
AGTGTCCAGCTGGAGACACCAATGTGACACCTCTTCAACAACAGAGCACAGGTCGACAGAGAAAACCTT
CACCTCCAGTGCATGATATAAAGCTGGGATCCCGGAATTTGATGAGTCTAAGAGACTCAAAAATCATCAT
TGGGTGTTTGTGGCCATCAACATCATGTGCTGACGATGCTGTGTCATTTTCTCAAGATGAGGAGACGACGCCA
CTGGCAAAACATCAGCCCAACAGGACTGTGAAATTTAATTTGATGTGATGAGATTACGGGAGACACCC
CATGGAAAGGCACATGCTGCCATGCTCTATCAGAGCATGAGCACTTAATCATATACATTCATATGATCTCCCTT
CAACCAACACACCAAGTTACACCAATAAATTCATACACAGTTCATGTCATACCGTTTAAATCTCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAACTTAAACATTTACAGAGTTACAAAAAACAAACATCAAAAAAAA
GACAGTTTATTTAAAGTACAACAATGACTGGCTTAATCTACTGTTTCAAAAAGTGTTCTTTTCAAAAAAACAA
AAAAAGAAAAAGAAATTTATTTTATAAATTTATTTGATGATCAAGACAGACAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSCVSCSNQFSKVIC
VRKNLREVPDGGISTNTRLNLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYNLAMLNLRREIPNLTPLIKDELDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCIDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGTMVTCMVSNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGP TPVVDWETNTVTTSLTPQ
STRSTKFTTIPVTDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

Parameter	Value	Unit	Reference
ρ_{air}	1.2	kg/m ³	[1]
ρ_{water}	1000	kg/m ³	[1]
ρ_{steel}	7850	kg/m ³	[1]
ρ_{concrete}	2400	kg/m ³	[1]
ρ_{glass}	2500	kg/m ³	[1]
ρ_{brass}	8500	kg/m ³	[1]
ρ_{copper}	8960	kg/m ³	[1]
ρ_{aluminum}	2700	kg/m ³	[1]
ρ_{polymer}	1200	kg/m ³	[1]
ρ_{rubber}	1100	kg/m ³	[1]
ρ_{foam}	30	kg/m ³	[1]
ρ_{ceramic}	3800	kg/m ³	[1]
ρ_{carbon}	2200	kg/m ³	[1]
ρ_{fiber}	1500	kg/m ³	[1]
ρ_{nanotube}	1300	kg/m ³	[1]
ρ_{graphene}	2200	kg/m ³	[1]
ρ_{silicon}	2330	kg/m ³	[1]
$\rho_{\text{germanium}}$	5320	kg/m ³	[1]
ρ_{gallium}	6040	kg/m ³	[1]
ρ_{indium}	7310	kg/m ³	[1]
ρ_{tin}	7280	kg/m ³	[1]
ρ_{lead}	11340	kg/m ³	[1]
ρ_{uranium}	19100	kg/m ³	[1]
$\rho_{\text{plutonium}}$	20250	kg/m ³	[1]
ρ_{mercury}	13540	kg/m ³	[1]
ρ_{gold}	19300	kg/m ³	[1]
ρ_{silver}	10490	kg/m ³	[1]
$\rho_{\text{palladium}}$	12020	kg/m ³	[1]
ρ_{nickel}	8850	kg/m ³	[1]
ρ_{iron}	7870	kg/m ³	[1]
ρ_{steel}	7850	kg/m ³	[1]
ρ_{aluminum}	2700	kg/m ³	[1]
ρ_{copper}	8960	kg/m ³	[1]
ρ_{brass}	8500	kg/m ³	[1]
ρ_{polymer}	1200	kg/m ³	[1]
ρ_{rubber}	1100	kg/m ³	[1]
ρ_{foam}	30	kg/m ³	[1]
ρ_{ceramic}	3800	kg/m ³	[1]
ρ_{carbon}	2200	kg/m ³	[1]
ρ_{fiber}	1500	kg/m ³	[1]
ρ_{nanotube}	1300	kg/m ³	[1]
ρ_{graphene}	2200	kg/m ³	[1]
ρ_{silicon}	2330	kg/m ³	[1]
$\rho_{\text{germanium}}$	5320	kg/m ³	[1]
ρ_{gallium}	6040	kg/m ³	[1]
ρ_{indium}	7310	kg/m ³	[1]
ρ_{tin}	7280	kg/m ³	[1]
ρ_{lead}	11340	kg/m ³	[1]
ρ_{uranium}	19100	kg/m ³	[1]
$\rho_{\text{plutonium}}$	20250	kg/m ³	[1]
ρ_{mercury}	13540	kg/m ³	[1]
ρ_{gold}	19300	kg/m ³	[1]
ρ_{silver}	10490	kg/m ³	[1]
$\rho_{\text{palladium}}$	12020	kg/m ³	[1]
ρ_{nickel}	8850	kg/m ³	[1]
ρ_{iron}	7870	kg/m ³	[1]
ρ_{steel}	7850	kg/m ³	[1]
ρ_{aluminum}	2700	kg/m ³	[1]
ρ_{copper}	8960	kg/m ³	[1]
ρ_{brass}	8500	kg/m ³	[1]
ρ_{polymer}	1200	kg/m ³	[1]
ρ_{rubber}	1100	kg/m ³	[1]
ρ_{foam}	30	kg/m ³	[1]
ρ_{ceramic}	3800	kg/m ³	[1]
ρ_{carbon}	2200	kg/m ³	[1]
ρ_{fiber}	1500	kg/m ³	[1]
ρ_{nanotube}	1300	kg/m ³	[1]
ρ_{graphene}	2200	kg/m ³	[1]
ρ_{silicon}	2330	kg/m ³	[1]
$\rho_{\text{germanium}}$	5320	kg/m ³	[1]
ρ_{gallium}	6040	kg/m ³	[1]
ρ_{indium}	7310	kg/m ³	[1]
ρ_{tin}	7280	kg/m ³	[1]
ρ_{lead}	11340	kg	

CGACGACGCTCTCAAGCTGCAACTCTGTGTGACAGTTGGCAGTTCTTTTCGGTTTCCCTCTGCTGTTTGGGGGCA
TGAAGAGGCTTTCCGCCGGGAGTAAAGAAAGGAATTGACCGGGCAGCGCAGGAGGAGCGCGCACGACCGC
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTGTGTCCGGCCGCGAGCGCGCGCTCGGTGGAGAGTTCCGGA
GACCTAGGCGCGCTGGACCGCGC**ATG**ACGCGCGCGAGAGCTCTCCGTGCGCGCGCCCGCGGGTTGGGGCTGCTGCTGTGC
CGCGTGTTCGGGGCGCGTCTGCGCGGTCCGACGAGCGCGTGTCCGGGAAGCTCGGCGACGCTCTGGGTGATCGCCG
GAGCGCCCATGCCCATCACTCTGCCGTCTGCTCGGGACCTGCTGGACTGCAGTCTGTAAGCGGCTAGCGCGCTCTT
CCCGAGCCACTCCGCTCTGGTCTCGCTGGCTGGACTTAAGTCAACAACAGATTATCTTTCATCAGAAGCAAGTCC
ATGAGCCACTCTCAAGCGCTTCGAGAGTGAATGAAACAACAAATGAATGGAGACCAATCCAAATCTGGGACA
GTCTCGGCAAGATATACACTTCTCTCTTGGCTGGAAACAGGATGTTGTTGAATACCTCCTTGAACATCTGAAAGAG
TTTAGTCCCTTGAATCTTTGGAACCTTAGCAGCAACAATATTACAGAGCTCAAATGTCATTTCCAGCCCTACA
CTCAAAATCTGTATCTCAACAGCAACCGAGTACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAAAC
CTCTTTGTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAAACTGCCCAACTGCCA
CATCTCGAATTGACCAAGAAACAAGATTAAAAATGTAGATGGAATGACATCCAGCGCTTGGTGCTCTGAAGTCT
CTGAAATGCAAGAAGATGGAGTAAAGAAATTTAGATGGAGCTTTTGGGGCTGAGCAACATCGAAATTTTG
CAGCTGGACCAATAACCACTTAACAGAGATTACCAAGAGCTGGCTTTACGGCTTGTGATGCTCGAGGAATTCAT
CTCAGCCAAATGGCATCAACAGGATCAGCCCTGATGCTCGGGAGTTCTGCCAAGACCTCAGTGAGCTGGAAC
ACTTTCATCACTTATCAAGGTTAGATGATCAAGCTCTCTTGGCTTAAGCTTACTAAATACATCTGCACATTGGG
AACAACAGAGTCAGCTACATTGCTGATTGTGCTTCTCGGGGGCTTTCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTTCTTGGATATTAAGACATAAAGATGTCCTTCTCGGGCTTGACAACATGAGGCATCTGATATCT
CAAGGAATCGGATCGTCTATTACTATAAGAAAGCTCTCAGTTTGGATGGATTTGGAGCATCTAGACCTGAGT
GACACGCAATCATGCTTTTCAAGGCAATGCAATTTACAATGAAGAAAGCTCAACAATTCGATTTAAATACA
TCAAGCTCTTTTGGCATTTGCCAGTCAAAATGGTCCCAACGTGGTGCGGGAACAACACTTTCAGAGCTTTGTA
AATGCCAGTTTGTGCCATCTCTCAGCTGCTAAAGGAAGAAGCATTTTGTGTTTGGCCAGATGGCTTTGTGT
GATGATTTTCCCAAAACCCAGATCACGGTTTCAGCCAGAACACAGTCCGGAAATAAAGGTTTCCAAATTTGAGTTT
ATCTGTCCTACGCTGCCAGCGAGCATGATTTCCCAATGCACTTTTGGCTGGGAATAAAGACATTTGAACATCTGATGAT
GCTGAAATGGAAATATGCAACACCTCGGGGCCAAGAGTGCGGAGGTGAGGATGATTAACCAACCTCTCTCGGCT
CGGAGGTGGAATTTGCCAGTGAAGGGAATATCAGTGTGTCATCTCAATCACTTTGGTTCATCTCTCTCTC
AAAGCCAAAGCTTCAGTAAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGC
ATGCCACGCTTGGAGTGTGCTGTGGTGGACCCAGCCGCCCCAGATGCTGCGCAAGGATGGGGCGACAGAC
TTCAGCTGCGACGGGAGAGCGCATGATGATGTGCCAGGATGACGTGCTTTTATCTGGATGTGAAGATA
GAGGACATTTGGGTATACAGCTGCCACAGCTCAGAAGAGTGAGGAAGTTTTCAGAAATAGCAACTCTGATGCTC
CTAGAAACCAACTCATTTTTCGGCGCACTGTGTGACCGAAGCTGAACAAAGGAGAAACAGCGCTCTCAGTGC
ATTGCTGGAGAGGCCCTCCCTTAACTGAATGAGCCAAAGATGATAGCCATTTGGTGGTAAACGAGAGGCCA
TTTTTTCAGCAGGCACTCAGCTTCTGATTTATTTGGACTCAGATGTGATGCTGGGAAATACCATGTGGAG
ATGCTTAACCCCTTGGCATGAGAGAGGAAAGCTCGCGCTCAGTGTGATCCCACTTCAACCTCGCATCTCCCT
CAGATGACAGCCCCATCGTTAGACATGACCGATGGGGCACTGTGGGTGTCTGATGATACAGCGCTTTGTGTT
GTGTGGGCGCTCAGTCTCGTGTGGGTGTCTCATATATACCAACAGCGGAGGAATGAAGATTGCAAGATTAC
AACACAGATGAGACCAACTTGCACAGATATCTCTAGTATTTGTCACTTCAGGGAAGCTTAGCTGACAGCGAG
GATGGGTGAGTGTCTTCAAGAAAGTGAAGGCCACCCAGATTGTGTCATCTCAGGTGTCTGGATTTCTTTACCA
CAACATGACAGTAGTGGGACCTTGCCATATTGCAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
TTTGTCCGTTTGGGATCCAGGCCCTATGATTTTGAAGGAAATGTGATGTGCTCAGATCTTTTGAACA
TATCATCAGGTTTGCAGTCTTGACCGAAGACAGCTTTTATGGACACAATTGAGCCGAGTACATAAAGAAAAG
GAGTGTCTACCCATGTTCTCATCTTCAAGAAAGACTCTGCGACCGAGGCTTCGATATATATCTGTGCGCTTCAT
TGAGGAGAGCTACTTAACATAGTTACTCTCAATGAGGAAGCTTGAATGAAATCTGTGTGTAACCAAGTCT
TCTTTAGATTCTTGACAAATCCAGAGCTAGGCTCGGTTGCTCGATGAATTTCTTTTGGGTATTTTGGAAA
GCTCTCAGGAGACCTACCTAGATGCCATTCAAGCTTTGGACAGCCCATCAGATTGTCAGCGCAGAGCGCTTTAT
TTGAAGGCTCATTTCTTCCCGAGCTTGACTCTGGGTGACGGAAGATGGGAAGAAGAGACAGATTTTCAGGA
GAAATACAATTGTGACCTTTTAAACAGACTTTAGAACACTACAGGACTCAAATTTTCACTCTTATGATCTGGAC
ACA**TAG**ACTGAATGAGGACAAAGGAAAGAGCTTAAACATACTACCTCAAGTGAACTTTATTTAAAGAGAGAGAAT
CTATGTTTTTTAAATGGAGTTTATGAATTTTAAAGAGCTAAATATGCTTTATTTATACAGATGAACCAAATTC
AAAAAGTTATGAATTTTTTATATCGGGAATGACTCATATAAGAATACCTTTTAAACTATTTTAAATCTTG
TTTTATGCAAAAAGTACTTTACGTAATTAATGATATAAATCATGATTTTATGATTTTATATATGCGACA
TTCTTTTATGGAATAAGTAGTTACTAAGAGCTTTTAAATATACCTGCTCTACCAATTTTATTAATGAGATT
ACTTCATTATTTTTCGACATATATTTTAAATATGTCATTTTGAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLSETLDDLSSNNISELQTAFFPALQLKYLNLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNISAI PPKMFKL PQLQHLELNRNKIKNV DGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWAEFC
QKLSLDELDTFNHLSRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNLTSSLLCDCQLKWLPPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDE
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDKNELLHDAEMENYAHRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETSPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF
FAAGNQLLIIVDSDDVSDAGKYTCEMSNTLGTERRGNVRLSVIPTPTCDSPQMTAPSLDDDDGWA
TVGVVIIAVVCCVGTSLVWVVIIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTADLRQ
DGYVSSSESGSHHQVFTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYSGDPFETYHTGCSPPDRPTVLMDDHYEPSYIKKKECYPCSHPSSESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSSLDFSANPEPASVASSNSFMGTGFKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQENHICTFKQTLNRYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCACGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGCTTTCGCGCTGTGGGGCGCGCTCGCGGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCATGGTGTGAACCGGGAGAGCCCTGGTGGTGGTCCCTATCCCTCCTTTATATA
GAAACCTTCCACACTGGGAAGGCACGCGCAGGCGAGGGGCTCATGGTGAAGGAGGCGCGGCTGATCTGCAG
GCGCACAGCATTCCGAGTTTACAGATTTTACAGATACCAAAATGGAAGGCGAGGAGGCGAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGGCGCCAGGCGCATCTGACTCGGCACCCCTGCGAGGACCATGGCCAGAGCCGGGTGCTGC
GTGCTCTGCTGCTGCTCGCGCCACAGCTGACCACTGGGACCTGTGCTTGGCGTGAAGGGCGCCAGGATTTGGCCGAA
TGGCGGCGCACAGCCTGAGCCCGCCGAGACGACAAACGAATTTGCGGAGGAGGAGCCGGTGTCTGATCTGAGCCCTGAGG
AGCCCGGGCTGGCCAGCCGCGGTGAGCTGCCCCGAGACTGTGCTGTTCAGGAGGGGCTGCTGGACTGTG
GCGGTATGACCTGCGTGAGTTCCCGGGGGACCTGCCTGAGCACCAACCACTATCTCTGCAGAACCAACAGC
TGGAAAAGATCTACCTGAGGAGCTCTCCGGGTGCACCGGTGGAGACACTGAACCTGCAAAACCAACCGCTGA
CTTCCCGAGGGCTCCAGAGAGGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAGC
TGACCTTGGCACCCTCTTCTGCCAAGCGCCCTGATCAGTGTGGACTTTGCTGCCAATATCTCACCAGATCT
ATGGGCTCACCTTTGCCAGAAAGCCAACTTGAGGTCTGTGTACTGCAACAACAAGCTGGCAGACGCCGGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCCTCATCTGTCCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCGCGCTGCCCTGTACAAAGCTGCACCTCAAGAACAAACAGCTGGAGAAGATCCCCCGGGGGCT
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACTACCTGACTGAGCAGGGGCTGGACAAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCTCAGCAACAACCTGTCTCGGCTCCGAGCTGGCTGC
CGCGCAGCCTGTGCTGCTGCTGCTGAGAGAAAGCGCATCCGGAGCGTGGAGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCAACGACCAACAGCTGCGGGAGCAGGCGATCCACCCTGGCCTTCCAGGGCT
TCAAGCGGTGACACGGTGCACCTGTACAAACGCGCTGGAGCGGTGCCAGTGGCTGCTGCGCGGCTGC
GCACCTCATGATCTGCAACAACAGATCAACGCGATTGGCCGCGAAGACTTGGCACCACTACTTCTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACGCGCCACAGGTGCACCGGAGCGCTTCCGCAAGCTGCGCTGCTGC
GCTCGCTGGACCTGTGCGGCAACCGGTGCACACGCTGCCACCTGGGCTGCCTGCAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCTTGGCACGAGGGGCGCTGCGGCGCATGGCTCAGCTGCGTGAAGCTGATCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCTGCTCTGGTGGACTCGCCCATCTGCAGCTGCTGGACA
TCGCGGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACTGCAGAACAA
AGATTAGTGGGTGCCCGCCAATGCTTGCAGCTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAGC
TGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGAGGCTGAAGCACTTCAGGTCTTGACATTGAAGGCACT
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAGGAGGAGGAAAGAGGAGGAGGAGG
AGGAAGAGGAAACAGATAGTGACAAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGAGCTCTTTCTGC
AGCACAGCTGTGCTGTGAGCCCGCATCTGCGGTGCTCACACAGACACACCAAGCTGCACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCTTCCACGGCGTGTCCACGGCCAGACACATGC
ACACATACACCCCTCAAACCCAGCTCAGCCACACACAACCTACCTCCAACCAACCAAGCTCTCTGTACAC
CCCCATACCGCTGCCACGCCCTTGAATCATGACGGGAAGGCTTGCCTTGCCTGGCACACAGGCACCCA
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACCAACACACACACATGCACAAGTCAATGTGCGAA
CAGCCCTCCAAGGCTATGCCACAGACAGCTCTTGGCCAGCCAGAATCAGCCATAGCAGCTGCGGCTGTGCCCT
GTCCATCTGTGCTCGTCCCTGGAGAAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCTGCCACCTCT
GGAATCACAAAAGCTGGCTTTTATCTTTTCCATCTATGGGGAAGGAGCTCAGGACTGCTGGCTGGCC
TGGCCCAACCTGCTCTCCAGGTGCTGGGCGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTTCAATGGGCAAGCCAGTGGAGGAGGATGGGAGAGCCCTGGGTGCTGCTGGGGCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGGCTGAGCCAGGGAAGGAGCAACAGCTGCACCTAGGAGACACCTT
GTTCTTCAGGCTGTGGGGGAAGTTCGGGTGCTTTATTTTATTTTATTTTCTAAGGAAAAAATGATAAAAAAT
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATAAAGCATTATCCCTATCCCTGCAAAAAA

FIGURE 108

MEGEEAEQPAWFHQPWRPGASDSAPPAGTMAQSRVLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPENEFABEEFVLVLSPEEFGPGPAAVSCPRDCACSQEGVVDCCGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPGAFSELSSRELYLQNNYLTDEGLDN
ETFWKLSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCTCGCCGCTGTCTCTCCGGAGCGGCAG
CAGTAGCCCCGGCGCGGAGGCTGGGGGTTCTTCGAGACTCTCAGAGGGGGCGCTCCCATCGGGCGCCACCACC
CAACTGTCTCTCGCGCGCACTGCGCTGGCGCCAGGACCCGCTGCCCAACTGGATTCTCTCTGGCGCTGGT
GCTGGTATCTCGCTCTACCTGACGGCGCGCGCGAGTTCGACGGGAGGTGGCCAGGCAATAGTGTATCGAT
TGGCCTATGTGTTATGGTGGGAGGATGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTACGCC
TGTGTGCCAACCAAGATGCAAAATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCTCTGGTATGGTGG
AAAAACCTGTATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGAAGCACAGGTGATGAACACTTA
CGGCAGCTTCAAGTGTCTACTGCTTCAACGGATATATGCTCATGCGGGATGGTCTCTGTCTCAAGTGCCCTGACCTG
CTCCATGCAAACTGTGATGATGGCTGTGATGTTGTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTATAAGGCTTCGATCTCATGTATATTGGAGG
CAAAATCAATGTGTATGACATAGACGAATGCTCACTTGGTCAAGTGTGACGAGCCTTGGCTCGATGTTATAA
CGTACGTGGGTCTTCAAGATGCAAAATGTAAAGAAGGATACAGGGTGTATGGAATGACTGTTGTGTATATCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTATGTATCCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTCTGATGTTGGAAGTACTTGGTGGCTCCGAAGACACATATATCTCTCTATCATTACCAA
CAGGCCCTACTTCTAAGCCAACAACAAGACCTACACCAAGCCAAACACCAATTCTCTACTCCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAAACCCGGACTGACAACTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGACCTCAGAAAACCCAGAGG
AGATGTGTTCAAGTGTCTGTGTACAGTTGTAATTTTGACCATGAGCTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAAATATCTGACAGTGTGCGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGTCTACTCTCGCCCGCTCATGCAATTCAGGGACCTGTGCTGTCTATTACGGCA
CAAGGTGACGGGGCTGCACCTCTGGCACCTCCAGGTGTTTGTGAGAAAACCGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCCTGGCTGGAGGCAAAACACAGATCACTTGGCAGGGGCTGACATCAAGAGGGAATCACA
AAGATGATTAAAGGGTTGGAAGAAAGATCTATGATGGAAGAAATTAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAAACCAATTGATGGTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACAGCTG
TTCTCCATATGCACTAAGAATAAGAACAGAGGAACTGGCTTAGACTAGATATAAGGGAGCATTTCTTGGCAGG
GGCCATGTTAGAACTCTCATAAAAAAGAGGTGTGAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA
TAAAAATTTGTCTATTTAAAGTGGTTAAAGATGTTCTTACCAGGAAAAAGTAAACAAATTATAGAATTTCCCAAA
AGATGTTTGTATCTACTAGTAGTATGCAAGTGAAGTCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CAATTCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAAGAGCCACCAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAATCCTAGCAGTATTAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTCAATGTTTCTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTCTTTTAAAGATCCTTCAAGGAACACAGTTCAGAGAG
ATTTTCATCGGGTGCAATTCCTCTGCTCTGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGGCCCTGCCCC
ACCCCGCAGACCTTTCCTCACCTACAGTATGATTGAGTTTCTCTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTGAACAATAGGTACAATAGAAGGTCTTCTGTCAATTAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAAATAAATCATTAAAGCCTTTGAGTAAACGGCAGAAATATATGGCTGTAGATCCATTTTAAATGGTTTCTT
TCCTTTATGGTATATACTGCAAGCTGAAGATGAAAGGGGAAATAAATGAAATTTTACTTTTTCGATGCCAA
TGATACATTGCACTAACTGATGGAAGAAGTTATCCAAAGTACTGTATAAATCTTGTGTTTATTTTAAATGTTT
CTAAAAATAAAATGTTAGTGGTTTCCAAATGGCCTAATAAAACAATTAATTTGTAATAAAAACTGTTAGTAAAT

FIGURE 110

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYQCDVVKGQIRQCPSPLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGLTKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTLRLTLPPTTTPERTTGLTTIAPAASPPGGITVDN
RVQTDPPQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLPGLRLMHSGLCLSFRLHKVTGLHSGTLQVFPVRKHGAHGAALWGRNGHGWRTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

[illegible]

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGA
AATGTGGCTCAAGGTTCTTCAACAACCTTTCTTTCCTTTGCAACAGGTGCTTGCTCGGGGCTGA
 AGGTGACAGTGCCATCACACACTGTCCATTGGCGTCAGAGTCAGGCCCTCTACCTACCCGCT
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTTGAGAGACCCCA
 CACAATGGCCAAATACTTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTGTACTTGGAAATACC
 AACACAAGTTTACCATTGATGCCACCCAATGCATCTCTGCTTATCAACCCCATCGACTTCCCT
 GATGAAGGCAATTTACATCGTGAAGGTCAACATTCAAGGAAATGGAACCTATCTGCGCAGTCA
 GAAGATACAAGTCACGGTTGATGATCCTGTGCACAAAGCCAGTGGTGCAGATTTCATCCTCCT
 CTGGGGCTCTGGAGTATGTGGGGAACATTGACCCGTGCACATCCGATTTGGAAGGGGGCACTCGG
 CTAGCTTTACCAATGGCTAAAAAATGGAGACCTGTCTCACACAGCTCCACCTACTCCTTTTC
 TCCCCAAAAACAATACCTTTCATATTGTCTCAGTAACCAAGGAAGACATTTGGGAATTACAGCT
 GCCTGTGTGAGGAACCCCTGTGCAGTGAAATGGAAGTGATATCATTATGCCCATCATATATTTAT
 GGACCTTATGGACTTCAAGTGAATTTGTATAAAGGGCTAAAAAGTAGGGGAAGTGTTTACTGT
 TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGTGATTCTCATCCCCCAACACCTACT
 CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTT
 GCATCTGAGAAGTAGGCCAGAGAACAATGGCATATGTGTGTCTGTCTTACACAACAATAAC
 CGGCAGGCAAGATGAACTCATTTCACAGTTATCATCTTCCGTAGGACTGAGAAGCTTG
 CACAGAAAGGAAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCATTATTTTGATT
 ATATCATGTGTCTTCTCTCCTTATGGAAAAAATATCAACCCATCAAGGTTATAAAAACAGAA
 ACTAGAAGGCGAGGCCAGAAACAGAATACAGGAAGCTCAAACTTTTCAGGCCATGAAGATG
 CTCTGGATGACTCTCGGAATATATGAATTTGTGCTTTTCCAGATGTTTCTGTGTTTCCAGG
 ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTGACAGGTACAGT
 GTATGAAGTTTATTCAGCACATCCCTGCCACGAGCAGAACCATTCAGAGTGA**ACT**TACATGG
 GCTAAACAGTCATCTCAGTGAATTTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAGT
 ATATTAACTTGAATCAGTGAAGAAACAGGACCAACACCTCTTACTCATTATTCCTTTACA
 TGCAGAAATAGAGCCATTTATGCAAAATGAACTCAGGTTTTTCAGCATATACAAATGCTTT
 GTGCAACAGAAAAACATGTTGGGAAATATTCCTAGTGGAGAGTCGTTCTCATGCTGACGG
 GGAGAACGAAAGTGACAGGGGTTTCCCTACAAGTTTGTATGAAATATCTCTACAAACCTCA
 ATTAGTCTACTCTACATCTTTCATATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
 TGTGGAAACTTTACATTGTTGATTTTTCAGCAGACTTGTGTTTTATTAATTTTATTATAGT
 TTAAGATGCTAAATTTATGTTTCAATTTTATTTTCCAAATTTCTATCTGTGTTATTGTGACAA
 CAAAGTAATAAGGATGTTGTCAAAAAACAAACATATGCCCTTCTCTTTTTTTTCAATCACC
 AGTAGTATTTTGAAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAGAGTCTTATTTT
 TTTTTTCAAGGAAGATGATTCAAATAAATTTATCTGTTTTTCTTTTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMMPNASLLINPLQFPDEGNYIVKVNIQGNGLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT
GRQDETHFTVIIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

[illegible]

GCAAGCGGCGGAAATGCGCCCTCCGGGAGTCTTGCAGTTCCTCCCTGGCAGTCTCGGTGCTGTT
GCTTTGGGGTGCTCCCTCGGAGCAGCGGGCGGGAGCAACGTTCCGCTCATCAGCGCAGAA
ACTCGAGAGAAGCTCGTGAAGGAGAGTGTATGAAATTTATGCCCCGGTGGCTCGCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGTCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCAAGAGCAGCCAGCACTAGCTGGACGCGTTTATCATACCTGCTC
TTCTCTACTATTTTACTTGAATGGTGAATTTAGCGCTATCAGGTCCAAGGACATAAG
AAGGACTTCATAAACTTTATAAGTGATAAGAGAGTGGAAAGATATTGAGCCCGTTTCATCAT
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGATGTCTCAGCACTCTTTACAGTATCTATGTGGA
TCAGGACGTCGCATAACTACTTTATTGAAGACCTTGGATTGCGAGTGGGGATCATATAC
GTTTGTGTTTAGCAACTCTGTTTCCGAGCTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCTTTTGTCTTCAAAAGGGCGCAGACCAGCCATACCCATACCTTTCAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAAACAAGAGCGGATGAAGAA
GATGTTTCAGAGAAGAAGCTGAAAGTAAAGAAGGAAACAAACAAGACTTTCCACAGAAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAAATCCTAGTTAAATTTTATAG
TTATCTTAATATATGATTTTGAATAAAAACAGAAAGATGATCATTTTGGTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCGAGGTTTCAGTCTAGATTGTCAATTAATTAAGAGTCTA
CATTCAAGACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAAGCAATAAGATTTATGATATTTGT
TTAATTAATAACCTAATTTCAAGCTGAGTTTGAATTTTCAATTTCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATATTTTAGAGAAAAATTTTCTCATTGATATAATTTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCCAATAAATGGGAAGTTTGCCCATCTGTCTCAAG
AAATGTGTATTTCAGTGACAATTTCTGTGCTCTTTTGAAGGTATATTCCAATTTCTCTGT
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTAACAGTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAAGTTCTAGGTATCTCTTGATTC
CAACAAAGTTTGATTTCTCTTGATTTTCTTACTTACTTACCTGGGTACATTTTATTTTT
CAAAATGGATGATAATTTCTTGGAACAATTTTTTAGTTTGTAGTAAACAGTATTTTTTGT
GTTTCAAAGTGAAGTTTACTGAGAGATCCATCAAATGAACAATCTGTTGTAATTTAAAT
TTGGCCACTTTTTCAGATTTTACATCTTTCTGCTGAACTTCAACTTGAATTTGTTTTT
TTTCTTTTGGATGTGAAGGTGAACATTTCTGATTTTGTCTGATGTGAAAGAGCTTTGGTA
TTTTACATTTTGAATTTCAAAGAAGCTTAATATAAAAGTTTGCAATCTACTCAGGAAAAAG
CATCTCTTGATATGCTCTAAAGTATTTTGTGCTCATATACAGAAAGTCTCTAAATGAT
TTTACAGTCTGTAAATGCTTGATGTTTAAAAATAATAAATTTTATATTTTTTAAAGACA
ACTTCATATTATCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTACAGGTAAAA
GTGAGTAGGATGGAACATTTTAGTGTATTTTACCTCTTAAAGAGCTAGAATACATAGTTTT
CACTTTAAAGAAGGGGAAAAATCATAAATAACAATGAATCACTGACCATTAGTAGTAGAC
AATTTCTGTAAGTGTCCCTCTCTTCTAGGCTCTGTGTGCTGTGAATCCATTAGATTTACAG
TATCGTAAATATACAAGTTTCTTTAAAGCCCTCTCTTTAGAATTTAAATATTGTACCAAT
AAAGAGTTTGGATGTGTAATCTGTGATGCTTAGAAAAATATCTTAAGCACAAAATAAACCT
TTCAACCACTCTATTAAAGCTGAAAAAATAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFI SDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCP SKRRRPQYPYP SKLLSESAQPLKKVEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIRQ RSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

[illegible]

TTAGGTGTGAGATGTTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTTAT
GGCATTTCCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSVCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALVDLQDSAGFIANLSVQRQFFP
TDEDEIGAALKALMRLQDITYRLDPGTISRGEPLGTTYQAMLSVDDCFGMGRSAYNEGDIYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEEREKTLTNQTEAELATPEGIYERPVDYLPDRDYESLCRGEVGLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASIRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDPS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSSEGIDYR
TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTVEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCTCTCTTTTCTAGTGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTATTATACCGTTTTCGGCTGGGGGTAGTTCCGACACCTTCACAGTTGAGAGACAGGACAGAGGAGTTGTGA
AGACAGGACAATCTCTTGGGGATGCTGGTCTCGGAAGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTTGACCC
CAGGTTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGGCACCACCTGGCAGGGCCTACCACCTAGCGACTGAGCTCCCTGTGTGGCTCTGCTGCGGCGAGCGGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTTCCCTGGATCCAGGGGGAGGAGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCCGGCTAGACCAAGTG
ATGAAGACTTCAAACCCCGGATTGTCCCTACTACAGGGACCCCAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTATCCAGACAGAGACTGGGCTCCCGTGAGCGGTGTGCTGGTGGCTGTCTGACCTCCCAGAGCTACACTGTCCA
CTTTGGCCGTGGCTGTGAACCGTACGCTGGCCCATCACTTCCTCGGTACTCTACTTCACTGGGCGAGCGGGGG
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGGCTCATGTCAAGAGACCTTC
GCCACCTTCAACACACTTTGGGGCCGACTACGACTGGTTCCTCATGTGAGGATGACACATATGTGACGGCCC
CCCGCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTCAATTG
GCGCAGGCGAGCAGGCCCCGTAAGTGTCTGATGGGGCTTTGGCTACCTGTGTGTGACGGAGTCTCCTGCTTCGTCTGC
GGCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCGTCTGACGAGTGGCTTGGACGCTGCCTCATTG
ACTCTCTGGGCTCGGCTGTGTCTCACAGCACCAGGGGCAGCAGTATCGCTCATTTGAACTGGCCAAAAATAGGG
ACCCCTGAGAAGGAAGGGAGCTCGGCTTTCTGAGTGCCCTTCGCCGTGCACCCCTGTCTCCGAAGGTACCCCTCATGT
ACCGGCTCCAAAAACGCTTCAGCGCTTGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACTGACGGCTCAGA
TCCGGAACCTGACCGTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGTCTCTTTCA
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCAAGAGCAGCACCTTCTCTGTGAGATGGGG
CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCGCTATCAGCCCCCGCTGCGCTTCCAGAAGCAGCGACTGTCAACGGCTATCGGCGCTTCGACCCAGCAC
GGGGCTGGAGTACACCTTGACCTGCTGTTGGAATGTGTGACACAGCTGGGCACCGCGGGCCCTGGCTCGCA
GGGTGAGCTGCTGCGGCTGCTGAGCCGGGTGGAATCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC
AGCTGGTGTGCTGCACTCTGCTGGCTGAAGCTGCTGCAGCCCCGGCTTTCCTCGAGGCGTTTGACGCCAATGTCC
TGGAGCCACGAGAACATGCTGCTCACCTGTGTGCTGTGCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG
ACCCATTCTTGGGGTGAAGCTGCGAGCAGCGGAGTTAGAGCGACGCTACCTGGGACGAGGCTGGCTGGCTGGCT
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGAAGTGGTCTCGAAGAAGCACCTTGTGGACACTCTCT
TCTTCTTACCACCGTGTGGAACAAGGCTGGGCCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT
GGCAGGCTCTTTCCAGTCCATTTCAGGAGTTCAATCCTGCCCTGTGACCAACAGAGATCAACCCACAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTCTGGTGTGACCCCTCCCGGGGGGCTTCTATAGGGGGGAGATTG
ACCGGCAGGCTTCTGCGGAGGCTGCTTCTACAAAGCTGACTACCTGGCGGCCGAGCAGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTCTCCTCGGTTCTCAGGGCTCC
ACCTCTTTCGGGCGTAGAGCCAGGGCTGGTGAGAAAGTTCTCCTGCGAGACTGCAGCCACGGCTCAGTGAAG
AACTCTACCACCGCTGCGGCTCAGCAACCTGGAGGGGCTAGGGGGCGTGCCAGGCTATGGCTCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCTGGGGGCCCTAACCTCATTACCTTCTCTTGTCTGCTCAGCC
CCAGGAAGGGCAAGCAAGATGGTGACAGATAGAGAAATGTTGTGCTGATTTTTTAAATATGAAATGTTATTAA
ACATGCTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLIILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPDSTRARLD
QSDQDFKPRIVPYYRDPNPKPYKKVLRTRYIQTELGSRELLLVAVLTSTRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWWFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHHRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLOQASRADVGDALLETALQNLNRRYQPRLRQKQRLNNGYR
RFDPARGMEYTTDLLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRYFG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGDPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMDFLRFSGSLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGLQAMALFEQEQA NST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

[illegible]

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLKKDPSQFFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLS I KEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACGCGTCCGATCTTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGGAGGAGAG
AAAAAGAGAGAGAGAGAGAAAACAAAAACCAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCTATTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
TTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAAGTAATTTGTTGTCATTGAACGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA
AACCTAAATGAGAGAGTTTTTTATTGGACTGTGAGACCAGGTTGTGCGAGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCTTGGAGGACTGTGCCACCATGAGAGACTTCTCAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTTCTCAATTATTTTCGATTGTGAAATGGTAGGAATAAATCCTTTG
AACAAAGGAAAAATCTCTTTAAAGAACAGAAAGGCACAACTCAAATGTGTAAGAAGGAAGAGCA
AGAACATGGCCACACCCACGCCCCACACGAGAAATTTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTTAAATGTTAAAAA
AAAAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLS DQVVEGQWVDGTP LTKSLSFWDVGE PNNIATLED CATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCGCGCTGGGCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTCGGCTCGGCTGCCTGACTCTCTCTGCTGCTGCTTTTCAGGGGCTGCGCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACCTGTCTGCATCATTTACGGATTGCG
AGACAAGTGAAGTGTGAGTGTGAGTGGGAAGAAATTCAGATGAACAAACCATATGTGTTTTTTGACAACAAAA
TTCAGGGAGACTTTGGCGGGTCTGTGCAAAATCTCGGGGAAGACATCCCTGAAGATCTGGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAATTTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGAACCCCTGTCTGTAGAGTGCCGAAGGCTGTACAGTAGGCAAGATGGCAACACTGTC
ACTGCGAGGAGTGTGAGGCCATCCCGCGGCTCACTACAGCTGGTATCGCAATGTATGATACCATGTCGCCAGCGATT
CCAGAGCCAATCCAGATTTTGCATTTCTTTTCCACTTAAACTCTGAAACAGGCACCTTTGGTGTTTCACTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCGAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGCTCCTTGTGTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAACCCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGACATACCTCTGTGAGAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTTTACTCTTAAAGAGCCCATGGAATAGAGAATTTTCTCAAGATGGACCCGGTAAATATAACCAAG
GGAAGCGAAACTGGGTGCGTTCTACTGAGTTGGGTTCTTAATCTGTTTCTGGCCGTGATTCGCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGTCTCAGCTAAAGCCCGGTGCTGGGCCCTGTGAAGCCAGCATGTTCAACCATGGTGCTT
CAGCAGCCACGACAGACCATGTGAGATGGCAGGTTGGCTGGACAGCACGAGCGCATTCGCGGCGGAACCCA
GAAAGGCTTTTACACAGACAGCTTACTTCTATCGGCCACAGACACCACCGCATTTCTTCTTAAAGGCTCTGTC
TGATCGGTGTGTCAGTGTCCATTGTCGAAGGAGCTTTTGGATCAGCATTTTGTAAAAACAAACAAATCAGGAAG
GTAATTTGGTTGCTGGAAGAGGATCTTGCCTGAGGAACCCCTGCTGTGTCACACAGGGGTGTCAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTGTTTATTTTATAAAATTT
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTAAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTTAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTATAAT
TGGAAAATATCAATAATTAAAGATATTTTACCACAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT
CACACAAGTTTATGCTTTTTCACAGGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAACCTT
TAAAAATTCAGATTAAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGTCTCTGGGGTTGCGCGAGGCCGCCCGCTCTAGCTCACTGTTGCCCTCGTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCTCCAGTGAGCTTTACTCAGCTGGCCCTTGCTTCTATCCAGCACAGC
TCTCAGGTGGGCACTGACGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAAACAGACCTG
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTGTGTTTAAATTAATTGTT
AAGATTGCTTAAGGCCAAAGGCAATTTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAAAGAAATGGAT
CCCCTGTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAAAGTCAAGGTGGAGCAGCCAGGTGAAAGGCTTGGCGGGGAGGAAAG
TGAAACGCCGTGAATCAAAGCAGTTTCTAATTTTGACTTTAAATTTTTCATCCGCGGAGACACTGCTGCCATT
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCTCATGTCCT
GCCGTGCTGACTCAGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTCGCTGGA
GAATGGCTCTCACTACTCACTTGTCTTTGAGCTTCCAGTGCTTGGGTTTTTATACTTTGACAGCTTTTTTTTT
AATTGCTACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAACACTTTTGCCGCGAGGCCGCTTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTT
CCTCCATCTATGCCACCTTGGTAGAGGGGATGGCTCCCCACCTCAGCGTTGGGGATTCACTGCTCCAGCCTCCT
TCTTGGTTGCTATAGTGTAGGGTAGCTTTATGCCCCCTCTTCTATACAAAACCTTCTACACTAGTGCCA
TGGGAACCAAGGTCTGAAAAAGTAGAGAGAGTGAAGTAGAGTCTGGGAAGTAGCTGCCATATACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTTAAAGATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTGCTGTACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCAATTTGTTTAAAC
CTCATTATATAAAGCTTCAAAAAACCCA

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FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFEDNKIQGDLGRAEILGKTSCLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267